

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 23:36:29 ; Search time 211 Seconds
(without alignments)
9073.778 Million cell updates/sec

Title: US-09-899-422A-1

Perfect score: 1368

Sequence: 1 atgggcctctccaccgtgcc.....Cgcccagttcttcagatga 1368

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1368	100.0	1368	9	US-09-898-234-1
2	1368	100.0	1368	9	US-09-899-429A-1
3	1368	100.0	1368	9	US-09-792-356-1
4	1368	100.0	1368	10	US-09-899-422-1
5	1368	100.0	2141	9	US-09-898-234-16
6	1368	100.0	2141	9	US-09-899-429A-26
7	1368	100.0	2141	9	US-09-792-356-16
8	1368	100.0	2141	10	US-09-899-422-16
9	1366.4	99.9	2111	10	US-09-880-107-2360
10	1366.4	99.9	2175	12	US-10-120-397-1
11	1363.2	99.6	1368	9	US-10-252-408-3
12	1122	82.0	1334	9	US-09-898-234-11
13	1122	82.0	1334	9	US-09-792-356-11
14	1122	82.0	1334	10	US-09-899-422-11
15	1117.2	81.7	1334	9	US-09-899-429A-21
16	743.4	54.3	2130	10	US-09-917-800A-1601
17	735.4	53.8	2173	9	US-09-898-234-14
18	735.4	53.8	2173	9	US-09-899-429A-24
19	735.4	53.8	2173	9	US-09-792-356-14

20	735.4	53.8	2173	10	US-09-899-422-14	Sequence 14, Appl
21	685.4	50.1	2440	10	US-09-970-532-1	Sequence 1, Appl
22	633	46.3	633	9	US-09-899-429A-7	Sequence 7, Appl
23	603	44.1	603	9	US-09-899-429A-13	Sequence 13, Appl
24	557	40.7	600	9	US-09-899-429A-11	Sequence 11, Appl
25	546	39.9	549	9	US-09-899-429A-9	Sequence 9, Appl
26	527	38.5	570	9	US-09-899-429A-17	Sequence 17, Appl
27	516	37.7	519	9	US-09-899-429A-15	Sequence 15, Appl
28	514	37.6	1301	10	US-09-756-186-7	Sequence 7, Appl
29	513	37.5	516	9	US-09-899-429A-19	Sequence 19, Appl
30	506	37.0	1147	10	US-09-756-186-5	Sequence 5, Appl
31	483	35.3	483	9	US-09-898-234-3	Sequence 3, Appl
32	483	35.3	483	9	US-09-899-429A-3	Sequence 3, Appl
33	483	35.3	483	9	US-09-792-356-3	Sequence 3, Appl
34	483	35.3	483	9	US-09-882-735-1	Sequence 1, Appl
35	483	35.3	483	10	US-09-899-422-3	Sequence 3, Appl
36	483	35.3	483	10	US-09-907-263-1	Sequence 1, Appl
37	483	35.3	486	9	US-09-899-429A-5	Sequence 5, Appl
38	479	35.0	479	9	US-10-043-487-100	Sequence 100, App
39	467	34.1	1674	9	US-09-359-595-12	Sequence 12, Appl
40	424.4	31.0	1049	10	US-09-756-186-1	Sequence 1, Appl
41	424.4	31.0	1202	10	US-09-756-186-3	Sequence 3, Appl
42	375.8	27.5	507	9	US-09-911-904-129	Sequence 129, App
43	337	24.6	427	10	US-09-876-889-236	Sequence 236, App
44	330	24.1	543	10	US-09-970-532-3	Sequence 3, Appl
45	329.6	24.1	5870	10	US-09-838-718A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-09-898-234-1
; Sequence 1, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-1
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1368)
; NAME/KEY: sig_peptide
; LOCATION: (1)..(87)
; NAME/KEY: misc_feature
; LOCATION: (88)..(120)
; OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
; NAME/KEY: misc_feature
; LOCATION: (606)..(633)
; OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by

US-09-898-234-1

[illegible]


```
QY 61 GGAATATACCCCTCAGGGGTTATTTGACTGTGTCCCTCACCCTAGGGGACAGGGAGAGAGA 120
DB 61 GGAATATACCCCTCAGGGGTTATTTGACTGTGTCCCTCACCCTAGGGGACAGGGAGAGAGA 120
QY 121 GATAGTGTGTGTCGCCCAAGGAAATATATCCACCCTCAAAATTAATTCGATTTCGTGTACC 180
DB 121 GATAGTGTGTGTCGCCCAAGGAAATATATCCACCCTCAAAATTAATTCGATTTCGTGTACC 180
QY 181 AAGTGCCACAAAGAACCTTACTTGTACAAATGACTGTCCAGGCCGCGGGCAGGATACGGAC 240
DB 181 AAGTGCCACAAAGAACCTTACTTGTACAAATGACTGTCCAGGCCGCGGGCAGGATACGGAC 240
QY 241 TGCAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAACACCTCAGACACTGCCCTC 300
DB 241 TGCAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAACACCTCAGACACTGCCCTC 300
QY 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAGATCTCTTCTTGCACAGTGGAC 360
DB 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAGATCTCTTCTTGCACAGTGGAC 360
QY 361 CGGGACACCGTGTGTGGCTGCGAGGAAGAACCACTACCGGCAATATTGGAGTGAACACCTT 420
DB 361 CGGGACACCGTGTGTGGCTGCGAGGAAGAACCACTACCGGCAATATTGGAGTGAACACCTT 420
QY 421 TTCCAGTGTCTCAATTGACAGCTCTGCCCTCAATGGAGCGTGCACCTCTCTCTGCCAGGAG 480
DB 421 TTCCAGTGTCTCAATTGACAGCTCTGCCCTCAATGGAGCGTGCACCTCTCTCTGCCAGGAG 480
QY 481 AAACAGAACACCGTGTGCACCTGCCATGTCAGTGTCTTCTTAAGAAACAGTGTGTTC 540
DB 481 AAACAGAACACCGTGTGCACCTGCCATGTCAGTGTCTTCTTAAGAAACAGTGTGTTC 540
QY 541 TCCTGTAGTAACTGTAAAGAAAGCCCTGAGTGCAGGAAGTGTGTCTACCCAGATTTGAG 600
DB 541 TCCTGTAGTAACTGTAAAGAAAGCCCTGAGTGCAGGAAGTGTGTCTACCCAGATTTGAG 600
QY 601 AATGTTAAGGACCTGAGGACCTCAGGCACCACTGCTGTGTGCTCCCTGTCTCAATTTCTTT 660
DB 601 AATGTTAAGGACCTGAGGACCTCAGGCACCACTGCTGTGTGCTCCCTGTCTCAATTTCTTT 660
QY 661 GGTCTTTGCTTTTATCCCTCTCTTTCATTGTTTAAATGCTATCGCTTACCAACGGTGAAG 720
DB 661 GGTCTTTGCTTTTATCCCTCTCTTTCATTGTTTAAATGCTATCGCTTACCAACGGTGAAG 720
QY 721 TCCAAAGCTCTACTCCTATTTTGTGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 780
DB 721 TCCAAAGCTCTACTCCTATTTTGTGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 780
QY 781 GGAAGCTACTAAGCCCTGCGCCGCAACCAAGCTTCAGTCCCACTCCAGCTTCACCTCACC 840
DB 781 GGAAGCTACTAAGCCCTGCGCCGCAACCAAGCTTCAGTCCCACTCCAGCTTCACCTCACC 840
QY 841 CCACCTCTGGCTTTCAGTCCCTGCGCCAGTTCACCTTCCAGCTTCCAGCTTCCAGCTTACC 900
DB 841 CCACCTCTGGCTTTCAGTCCCTGCGCCAGTTCACCTTCCAGCTTCCAGCTTCCAGCTTACC 900
QY 901 CCGGTGACTGTCCCAACTTTGGGCTCCCGCAGAGAGTGGCACCACCTTATCAGGGG 960
DB 901 CCGGTGACTGTCCCAACTTTGGGCTCCCGCAGAGAGTGGCACCACCTTATCAGGGG 960
QY 961 GGTGACCCCATCTTTCGACAGCCCTTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1020
DB 961 GGTGACCCCATCTTTCGACAGCCCTTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1020
QY 1021 TGGGAGGACGCGCCACAGCCACAGAGCTTACAGCTGATGACCCCGGAGCTGTAC 1080
DB 1021 TGGGAGGACGCGCCACAGCCACAGAGCTTACAGCTGATGACCCCGGAGCTGTAC 1080
QY 1081 GCGGTGTTGGAAGACCTGCCCCGTTGCGCTTGAAGAAATTCGTGGCGGCGCTTAGGGCTG 1140
DB 1081 GCGGTGTTGGAAGACCTGCCCCGTTGCGCTTGAAGAAATTCGTGGCGGCGCTTAGGGCTG 1140
```

```
QY 1141 ACCGACCAGGATCGATCGCTGGCTGGAGCTGCAGAACGGGCGCTGCTGCGGAGGCGCAA 1200
DB 1141 ACCGACCAGGATCGATCGCTGGCTGGAGCTGCAGAACGGGCGCTGCTGCGGAGGCGCAA 1200
QY 1201 TACAGCATGCTGGGACCTTGGAGGGCGCACCGCGCGGAGGCCACGCTGGAGCTG 1260
DB 1201 TACAGCATGCTGGGACCTTGGAGGGCGCACCGCGCGGAGGCCACGCTGGAGCTG 1260
QY 1261 CTGGACGCGCTCTCCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGAGCG 1320
DB 1261 CTGGACGCGCTCTCCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGAGCG 1320
QY 1321 CTTTGGGCGCGCGCGCGCTCCCGCGCGCGCGCTCTCTCTCAGATGA 1368
DB 1321 CTTTGGGCGCGCGCGCGCTCCCGCGCGCGCGCTCTCTCTCAGATGA 1368
```

RESULT 5

```
US-09-898-234-16
; Sequence 16, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98,385-1
; CURRENT APPLICATION NUMBER: US/09/898,234
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2141
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213)...(1580)
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
; OTHER INFORMATION: ITNF-R2
US-09-898-234-16
```

```
Query Match 100.0%; Score 1368; DB 9; Length 2141;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCTCTCCACCGTCTGACCTGCTGCCACTGCTGCCACTGCTGCTGCTGCTGCTG 60
DB 213 ATGGGCTCTCCACCGTCTGACCTGCTGCCACTGCTGCCACTGCTGCTGCTGCTG 272
QY 61 GGAATATACCCCTCAGGGGTTATTTGACTGTGTCCTCACCCTAGGGGACAGGAGAGA 120
DB 273 GGAATATACCCCTCAGGGGTTATTTGACTGTGTCCTCACCCTAGGGGACAGGAGAGA 332
QY 121 GATAGTGTGTGTCGCCCAAGGAAATATATCCACCCTCAAAATTAATTCGATTTCGTGTACC 180
DB 333 GATAGTGTGTGTCGCCCAAGGAAATATATCCACCCTCAAAATTAATTCGATTTCGTGTACC 392
QY 181 AAGTGCCACAAAGAACCTTACTTGTACAAATGACTGTCCAGGCCGCGGGCAGGATACGGAC 240
DB 393 AAGTGCCACAAAGAACCTTACTTGTACAAATGACTGTCCAGGCCGCGGGCAGGATACGGAC 452
```

```
QY 241 TGCAGGAGTGTGAGAGCGGCTCCCTTCACCGCTTCAGAAAAACCACTCCTCAGACACTGCCTC 300
Db 453 TGCAGGAGTGTGAGAGCGGCTCCCTTCACCGCTTCAGAAAAACCACTCCTCAGACACTGCCTC 512
QY 301 AGCTGCTCCAATGCCGAAAGAAATGGGTGAGTGGAGATCTCTTCTTGACAGTGGAC 360
Db 513 AGCTGCTCCAATGCCGAAAGAAATGGGTGAGTGGAGATCTCTTCTTGACAGTGGAC 572
QY 361 CGGACACCGTGTGGCTGCAGGAAGAACAGTACCGGCATTTATGGAGTGAACACTT 420
Db 573 CGGACACCGTGTGGCTGCAGGAAGAACAGTACCGGCATTTATGGAGTGAACACTT 532
QY 421 TTCAGTGTCTCAATGTCAGCTCTGCTCAATGGGACCGTGCACCTCTCTGCGAGGAG 480
Db 633 TTCAGTGTCTCAATGTCAGCTCTGCTCAATGGGACCGTGCACCTCTCTGCGAGGAG 692
QY 481 AAACAGACACCGTGTGCACCTGCCATGCATGCGAGTTTCTTCTTAAGAGAAAACAGTGTGC 540
Db 693 AAACAGACACCGTGTGCACCTGCCATGCATGCGAGTTTCTTCTTAAGAGAAAACAGTGTGC 752
QY 541 TCCTGTAGTAAGTAAAGAAAGCTGGAGTGCAGAGTTGTGCTACCCAGATTGAG 600
Db 753 TCCTGTAGTAAGTAAAGAAAGCTGGAGTGCAGAGTTGTGCTACCCAGATTGAG 812
QY 601 AATGTTAAGGCACTGAGGACTCAGGCACCAAGTGTGTTGCCCTGGTCAATTTCTTT 660
Db 813 AATGTTAAGGCACTGAGGACTCAGGCACCAAGTGTGTTGCCCTGGTCAATTTCTTT 872
QY 661 GGTCTTTGCCCTTTATCCCTCTCTTCATTTGGTTTAATGTATCGTACCAACGGTGGAG 720
Db 873 GGTCTTTGCCCTTTATCCCTCTCTTCATTTGGTTTAATGTATCGTACCAACGGTGGAG 932
QY 721 TCCAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGA 780
Db 933 TCCAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGA 992
QY 781 GGAAGTCTACTAAGCCCTTGCCGCCAAACCCAAAGTTCAGTCCCACTCCAGGTTTACC 840
Db 993 GGAAGTCTACTAAGCCCTTGCCGCCAAACCCAAAGTTCAGTCCCACTCCAGGTTTACC 1052
QY 841 CCCACCTGGGCTTCAGTCCCGTCCGAGTTCAGCTTCACCTCCAGTCCACCTATACC 900
Db 1053 CCCACCTGGGCTTCAGTCCCGTCCGAGTTCAGCTTCACCTCCAGTCCACCTATACC 1112
QY 901 CCCGTGACTCTCCAACTTTGCGGCTCCCGCAGAGAGTGGACCACTATCAGGGG 960
Db 1113 CCCGTGACTCTCCAACTTTGCGGCTCCCGCAGAGAGTGGACCACTATCAGGGG 1172
QY 961 GCTGACCCCATCTTTGGACAGCCCTGCGCTCCGACGCCATCCCAACCCCTTCAGAG 1020
Db 1173 GCTGACCCCATCTTTGGACAGCCCTGCGCTCCGACGCCATCCCAACCCCTTCAGAG 1232
QY 1021 TGGGAGGACAGCGCCCAAGCCACAGAGCTAGACATGATGATACCCCGCAGCTCTAC 1080
Db 1233 TGGGAGGACAGCGCCCAAGCCACAGAGCTAGACATGATGATACCCCGCAGCTCTAC 1292
QY 1081 GCCGTGTGGAGAACGTGCCCGCTTGGCTGGAGGAATTCGTGCGCGCGCTAGGGCTG 1140
Db 1293 GCCGTGTGGAGAACGTGCCCGCTTGGCTGGAGGAATTCGTGCGCGCGCTAGGGCTG 1352
QY 1141 AGCAGACAGAGATCGATCGGCTGGAGTGCAGAACGGGCGCTGCTGCGCGAGCGCAA 1200
Db 1353 AGCAGACAGAGATCGATCGGCTGGAGTGCAGAACGGGCGCTGCTGCGCGAGCGCAA 1412
QY 1201 TACAGCATGCTGGGACCTGAGGCGGCGACCGCGCGGCGAGGCCACCGCTGAGCTG 1260
Db 1413 TACAGCATGCTGGGACCTGAGGCGGCGGACCGCGCGGCGAGGCCACCGCTGAGCTG 1472
QY 1261 CTGGAGCGCTGCTCCCGACATGAGACTGCTGCGGCTGCTGAGGAGCATCGAGAGGCG 1320
Db 1473 CTGGAGCGCTGCTCCCGACATGAGACTGCTGCGGCTGCTGAGGAGCATCGAGAGGCG 1532
```

```
QY 1321 CTTTGGCGCCCGCGCCCTCCCGCCCGCCCGCCAGTCTTCTTCAGATGA 1368
Db 1533 CTTTGGCGCCCGCGCCCTCCCGCCCGCCCGCCAGTCTTCTTCAGATGA 1580

RESULT 6
US-09-899-429A-26
; Sequence 26, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2141
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
; OTHER INFORMATION: TNF-R2
; NAME/KEY: CDS
; LOCATION: (213)..(1577)
US-09-899-429A-26

Query Match 100.0%; Score 1368; DB 9; Length 2141;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGTCTCTGGAGCTGTGGTG 60
Db 213 ATGGGCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGTCTCTGGAGCTGTGGTG 272
QY 61 GGAATATACCCCTCAGGGTTATTGGACTGGTGTCTCCTCAGTGGGACAGGAGAGA 120
Db 273 GGAATATACCCCTCAGGGTTATTGGACTGGTGTCTCCTCAGTGGGACAGGAGAGA 332
QY 121 GATAGTGTGTCTCCCAAGGAAATATATCCACCTCAAAATAATTGGATTGTGTACC 180
Db 333 GATAGTGTGTCTCCCAAGGAAATATATCCACCTCAAAATAATTGGATTGTGTACC 392
QY 181 AAGTGCACAAAGAACCTACTTGTACAACTGTGTCCAGCCCGGGGACAGGATACGGAC 240
Db 393 AAGTGCACAAAGAACCTACTTGTACAACTGTGTCCAGCCCGGGGACAGGATACGGAC 452
QY 241 TGCAGGAGTGTGAGAGCGGCTCTTCCAGCTTCAGAAAACCACTCAGACACTGCCTC 300
Db 453 TGCAGGAGTGTGAGAGCGGCTCTTCCAGCTTCAGAAAACCACTCAGACACTGCCTC 512
QY 301 AGCTGCTCCAATGCCGAAAGAAATGGGTGAGTGGAGATCTCTTCTTGACAGTGGAC 360
Db 513 AGCTGCTCCAATGCCGAAAGAAATGGGTGAGTGGAGATCTCTTCTTGACAGTGGAC 572
QY 361 CGGACACCGTGTGAGTGGCTGCAGGAAGAACAGTACCGGCATTTATGGAGTGAACACTT 420
```


QY	1081	GCCTGGTGGAGAACGTGCCCCCGCTTGGAGGAATTCGTGGCGGCCCTAGGGCTG	1140
Db	1336	GCCTGGTGGAGAACGTGCCCCCGCTTGGAGGAATTCGTGGCGGCCCTAGGGCTG	1395
QY	1141	AGCGACACAGATCGATCGGTGGAGCTGAGACGGCGCTGCTGCGGAGGCGCAA	1200
Db	1396	AGCGACACAGATCGATCGGTGGAGCTGAGACGGCGCTGCTGCGGAGGCGCAA	1455
QY	1201	TACAGCATCTGGCGACCTGGAGGGGGCGACCGCGCGGCGAGGCCACGCTGGAGCTG	1260
Db	1456	TACAGCATCTGGCGACCTGGAGGGGGCGACCGCGCGGCGAGGCCACGCTGGAGCTG	1515
QY	1261	CTGGGAGCGTCTCCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGAGGGG	1320
Db	1516	CTGGGAGCGTCTCCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGAGGGG	1575
QY	1321	CTTTGGGGCCGCGCCCTCCGCGCCGCCAGTCTTCACATGA	1368
Db	1576	CTTTGGGGCCGCGCCCTCCGCGCGCGCCAGTCTTCACATGA	1623

RESULT 11

```

RESOLUTION 11
US-10-252-408-3
; Sequence 3, Application US/10252408
; Publication NO. US20030082736A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, CRAIG A.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND BETA-RECEPTORS
; FILE REFERENCE: A-71592
; CURRENT APPLICATION NUMBER: US/10/252,408
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US/08/406,824
; PRIOR FILING DATE: 1995-03-20
; PRIOR APPLICATION NUMBER: US 08/255,849
; PRIOR FILING DATE: 1994-06-08
; PRIOR APPLICATION NUMBER: US 07/860,710
; PRIOR FILING DATE: 1992-03-30
; PRIOR APPLICATION NUMBER: US 07/523,635
; PRIOR FILING DATE: 1990-05-10
; PRIOR APPLICATION NUMBER: US 07/421,417
; PRIOR FILING DATE: 1989-10-13
; PRIOR APPLICATION NUMBER: US 07/405,370
; PRIOR FILING DATE: 1989-09-11
; PRIOR APPLICATION NUMBER: US 07/403,241
; PRIOR FILING DATE: 1989-09-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ. ID. NO. 1

```

Query Match	99.6%	Score 1363.2	DB 9	Length 1368
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1365	Conservative	0	Mismatches	0
		3	Indels	0
			Gaps	0

[illegible]

QY 1141 AGCGACCGAGATCGATCGGCTGGAGCTGCAGAACGGCGCTGCTCGCGAGCGCA 1200
|||||
Db 1141 AGCGACCGAGATCGATCGGCTGGAGCTGCAGAACGGCGCTGCTCGCGAGCGCA 1200
|||||
QY 1201 TACAGCATGCTGGCGACCTGGAGCGCGCGACCGCGCGCGCGCGCGCGCGCGCG 1260
|||||
Db 1201 TACAGCATGCTGGCGACCTGGAGCGCGCGACCGCGCGCGCGCGCGCGCGCGCG 1260
|||||
QY 1261 CTGGACCGCTGCTCCGCGACATGAGCCTGCTGGGCTGCCCTGGAGGACATCGAGGCG 1320
|||||
Db 1261 CTGGACCGCTGCTCCGCGACATGAGCCTGCTGGGCTGCCCTGGAGGACATCGAGGCG 1320
|||||
QY 1321 CTTTGGCGCGCGCGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
|||||
Db 1321 CTTTGGCGCGCGCGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
|||||

RESULT 12

US-09-898-234-11
; Sequence 11, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98,385-1
; CURRENT APPLICATION NUMBER: US/09/898,234
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213)..(1325)
; OTHER INFORMATION: Description of Artificial Sequence: cDNA insert of
; OTHER INFORMATION: lambdaTNF-Bp15 and pTNF-Bp15 vectors
US-09-898-234-11

Query Match 82.0%; Score 1122; DB 9; Length 1334;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGCGCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCCTCCTGGAGCTGTGGTG 60
|||||
Db 213 ATGGGCGCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCCTCCTGGAGCTGTGGTG 272
|||||
QY 61 GGAATATACCCCTCAGGCGTTATTGGAGCTGCTCCCTCACCTAGGGGACAGGAGAAGA 120
|||||
Db 273 GGAATATACCCCTCAGGCGTTATTGGAGCTGCTCCCTCACCTAGGGGACAGGAGAAGA 332
|||||
QY 121 GATAGTGTGTCCCGCAAGGAAATATATCCACCTCAAAATAATTCGATTGTGTAC 180
|||||
Db 333 GATAGTGTGTCCCGCAAGGAAATATATCCACCTCAAAATAATTCGATTGTGTAC 392
|||||
QY 181 AAGTGCCCAAGGAACCTACTTGTACATGACTGTCCAGCGCGCGCGCGCGCGCGCGCG 240
|||||
Db 393 AAGTGCCCAAGGAACCTACTTGTACATGACTGTCCAGCGCGCGCGCGCGCGCGCGCG 452
|||||

QY 241 TCGAGGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAACACCTCAGACACTGCCTC 300
|||||
Db 453 TCGAGGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAACACCTCAGACACTGCCTC 512
|||||
QY 301 AGCTGCTCCAAATGCCGAAGAAATGGTGTAGGTGGAGATCTCTTCTTGCACAGTGAC 360
|||||
Db 513 AGCTGCTCCAAATGCCGAAGAAATGGTGTAGGTGGAGATCTCTTCTTGCACAGTGAC 572
|||||
QY 361 CGGGACACCGTGTGGCTGCAGGAAGAACACAGTACCGGCATTATTGGAGTCAAAACCTT 420
|||||
Db 573 CGGGACACCGTGTGGCTGCAGGAAGAACACAGTACCGGCATTATTGGAGTCAAAACCTT 632
|||||
QY 421 TTCCAGTGTCTCAATTGACGCTCTGCTCAATGGGACCGTGCACCTCTCTCTGCCAGGAG 480
|||||
Db 633 TTCCAGTGTCTCAATTGACGCTCTGCTCAATGGGACCGTGCACCTCTCTCTGCCAGGAG 692
|||||
QY 481 AAACAGACACCGTGTGCACCTGCCATGCGAGTTTCTTTCTAAGAGAAACAGTGTGTC 540
|||||
Db 693 AAACAGACACCGTGTGCACCTGCCATGCGAGTTTCTTTCTAAGAGAAACAGTGTGTC 752
|||||
QY 541 TCCTGTAGTAACTGTAAGAAAGCCCTGGAGTGCACGAAAGTTGCTGCTACCCAGATTGAG 600
|||||
Db 753 TCCTGTAGTAACTGTAAGAAAGCCCTGGAGTGCACGAAAGTTGCTGCTACCCAGATTGAG 812
|||||
QY 601 AATGTTAAGGACACTGAGGACTCAGGCACACAGTGTGTTGCCCTGCTCATTTCTTT 660
|||||
Db 813 AATGTTAAGGACACTGAGGACTCAGGCACACAGTGTGTTGCCCTGCTCATTTCTTT 872
|||||
QY 661 GGTCTTTGCCCTTTATCCCTCTCTCTCATTTGGTTAAATGTATCGCTACCAAGTGGAG 720
|||||
Db 873 GGTCTTTGCCCTTTATCCCTCTCTCTCATTTGGTTAAATGTATCGCTACCAAGTGGAG 932
|||||
QY 721 TCCAACTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGAGGGGAGCTTGAA 780
|||||
Db 933 TCCAACTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGAGGGGAGCTTGAA 992
|||||
QY 781 GGAATCTACTAAGCCCTTGCCGCCAAACCCAAAGCTTCAGTCCACCTCCAGCTTACC 840
|||||
Db 993 GGAATCTACTAAGCCCTTGCCGCCAAACCCAAAGCTTCAGTCCACCTCCAGCTTACC 1052
|||||
QY 841 CCCACCTGGGCTTCAGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGT 900
|||||
Db 1053 CCCACCTGGGCTTCAGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGT 1112
|||||
QY 901 CCCGTGACTGTCCCAACTTTTGGGCTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGT 960
|||||
Db 1113 CCCGTGACTGTCCCAACTTTTGGGCTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGT 1172
|||||
QY 961 GCTGACCCCTCTCTTGGCAGACGCTCGCTCCGACCCCATCCCAACCCCTTCCAGAG 1020
|||||
Db 1173 GCTGACCCCTCTCTTGGCAGACGCTCGCTCCGACCCCATCCCAACCCCTTCCAGAG 1232
|||||
QY 1021 TGGGAGGACAGCGGCCCAAGCCACAGACCTTAGACACTGATGACCCCGGACGCTGTAC 1080
|||||
Db 1233 TGGGAGGACAGCGGCCCAAGCCACAGACCTTAGACACTGATGACCCCGGACGCTGTAC 1292
|||||
QY 1081 GCCGTGTGGAGAGAGTGCCTCCGCTGGGAGGAAATTC 1122
|||||
Db 1293 GCCGTGTGGAGAGTGCCTCCGCTGGGAGGAAATTC 1334
|||||

RESULT 13

US-09-792-356-11
; Sequence 11, Application US/09792356
; Publication No. US20020183485A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them

FILE REFERENCE: 98,385-G
CURRENT APPLICATION NUMBER: US/09/792,356
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 08/477,639
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/383,676
PRIOR FILING DATE: 1995-02-01
PRIOR APPLICATION NUMBER: 08/153,287
PRIOR FILING DATE: 1993-11-17
PRIOR APPLICATION NUMBER: 07/821,750
PRIOR FILING DATE: 1992-01-02
PRIOR APPLICATION NUMBER: 07/511,430
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 1334
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (213)..(1325)
OTHER INFORMATION: Description of Artificial Sequence: cDNA insert of
; OTHER INFORMATION: lambdaTNF-BP15 and pTNF-BP15 vectors
US-09-792-356-11

Query Match 82.0%; Score 1122; DB 9; Length 1334;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGCGCTCTCCACCGTGGCTGACCTGCTGCTGCCACCTGGTGTCTCTCTGGAGCTGTGGTG 60
DB 213 ATGGGCGCTCTCCACCGTGGCTGACCTGCTGCTGCCACCTGGTGTCTCTCTGGAGCTGTGGTG 272

QY 61 GGAATATACCCCTCAGGGGTTATTGGACTGGTTCCTCCTACCTAGGGGACAGGAGAGAGA 120
DB 273 GGAATATACCCCTCAGGGGTTATTGGACTGGTTCCTCCTACCTAGGGGACAGGAGAGAGA 332

QY 121 GATAGTGTGTGTCGCCAAGGAAATATATCCACCTCAAAATATTCGATTTGCTGTACC 180
DB 333 GATAGTGTGTGTCGCCAAGGAAATATATCCACCTCAAAATATTCGATTTGCTGTACC 392

QY 181 AAGTCCCAAGGAACTACTTGTACATGACTGTCCAGGCGCGGGGCGGAGATACGGAC 240
DB 393 AAGTCCCAAGGAACTACTTGTACATGACTGTCCAGGCGCGGGGCGGAGATACGGAC 452

QY 241 TCAGGGAGTGTGAGAGCGGCTCTTCCAGGCTTCAGAAACACCTCAGACACTGCCCTC 300
DB 453 TCAGGGAGTGTGAGAGCGGCTCTTCCAGGCTTCAGAAACACCTCAGACACTGCCCTC 512

QY 301 AGCTGCTCCAAATGCCGAAGAAATGGGTCAAGTGGAGATCTCTTTTCACAGTGGAC 360
DB 513 AGCTGCTCCAAATGCCGAAGAAATGGGTCAAGTGGAGATCTCTTTTCACAGTGGAC 572

QY 361 CGGGACACCGTGTGGCTGCAGGAGAACACAGTACCGGCATATTGGAGTGAACACCTT 420
DB 573 CGGGACACCGTGTGGCTGCAGGAGAACACAGTACCGGCATATTGGAGTGAACACCTT 632

QY 421 TTCAGTGTCTCAATTTGACGCTCTTCCCTCAATGGACCGTCCCTCTCTCTCCAGGAG 480
DB 633 TTCAGTGTCTCAATTTGACGCTCTTCCCTCAATGGACCGTCCCTCTCTCTCCAGGAG 592

QY 481 AAACGAACACCGTGTGACCTGCCATGCCAGTGTCTTTTCTAAGAGAAACAGTGTGTC 540
DB 693 AAACGAACACCGTGTGACCTGCCATGCCAGTGTCTTTTCTAAGAGAAACAGTGTGTC 752

QY 541 TCCTGTAGTAACTTAAGAAAGCTTGGAGTGCAGAGTGTGCTTACCCAGATTTAG 600
DB 753 TCCTGTAGTAACTTAAGAAAGCTTGGAGTGCAGAGTGTGCTTACCCAGATTTAG 812

QY 601 AATGTTAAGGGCCTGAGGACTCAGGACACAGTGTCTGTCCTGCTGCTATTTCTTTT 660
DB 813 AATGTTAAGGGCCTGAGGACTCAGGACACAGTGTCTGTCCTGCTGCTATTTCTTTT 872

QY 661 GGTCTTTGCTTTTATCCTCTCTCTTCAATTTGTTAATGCTATCGCTACCAACGGTGAAG 720
DB 873 GGTCTTTGCTTTTATCCTCTCTCTTCAATTTGTTAATGCTATCGCTACCAACGGTGAAG 932

QY 721 TCCAAGCTCTACTCTCATTTGTTGGGAATCGACACCTGAAAGAGAGGGGAGCTTGAA 780
DB 933 TCCAAGCTCTACTCTCATTTGTTGGGAATCGACACCTGAAAGAGAGGGGAGCTTGAA 992

QY 781 GGAAGTACTACTAAGCCCTGCGCCCAACCAAGCTTCAGTCCCACTCCAGGCTTCACC 840
DB 993 GGAAGTACTACTAAGCCCTGCGCCCAACCAAGCTTCAGTCCCACTCCAGGCTTCACC 1052

QY 841 CCCACCTGGGCTTCAGTCCCTGGCCAGTTCACACTTCACCTCCAGCTTCACCTATACC 900
DB 1053 CCCACCTGGGCTTCAGTCCCTGGCCAGTTCACACTTCACCTCCAGCTTCACCTATACC 1112

QY 901 CCCGGTGAAGTCCCAACTTTGGGCTCCCGCAGAGAGTGGCAGCCACCTATCAGGGG 960
DB 1113 CCCGGTGAAGTCCCAACTTTGGGCTCCCGCAGAGAGTGGCAGCCACCTATCAGGGG 1172

QY 961 GCTGACCCCATCTTCGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1020
DB 1173 GCTGACCCCATCTTCGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1232

QY 1021 TGGGAGGACAGCGCCCAAGCCACAGCCCTAGACACTGATGACACCCCGAGCGCTGTAC 1080
DB 1233 TGGGAGGACAGCGCCCAAGCCACAGCCCTAGACACTGATGACACCCCGAGCGCTGTAC 1292

QY 1081 GCGGTGGTGGAGACGTGCCCCCGTTGCGCTGGAAGGAATTC 1122
DB 1293 GCGGTGGTGGAGACGTGCCCCCGTTGCGCTGGAAGGAATTC 1334

RESULT 14

US-09-899-422-11
; Sequence 11, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213)..(1325)
; OTHER INFORMATION: Description of Artificial Sequence: cDNA insert of
; OTHER INFORMATION: lambdaTNF-BP15 and pTNF-BP15 vectors
US-09-899-422-11

Query Match 82.0%; Score 1122; DB 10; Length 1334;
Best Local Similarity 100.0%; Pred. No. 0;

361	QY	CGGGACACCGTGTGGCTGCAGAGAAGACCACTACCGCGATTATTGGAGTGAACACCTT	420
573	Db	CGGGACACCGTGTGGCTGCAGAGAAGACCACTACCGCGATTATTGGAGTGAACACCTT	632
421	QY	TTCCAGTGCCTTCAATTGCAGCCCTGCCTCAATGGGACCGTGCACTCTCCTGCCAGGAG	480
633	Db	TTCCAGTGCCTTCAATTGCAGCCCTGCCTCAATGGGACCGTGCACTCTCCTGCCAGGAG	692
481	QY	AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTTAAGAGAAAAACGAGTGTGC	540
693	Db	AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTTAAGAGAAAAACGAGTGTGC	752
541	QY	TCCTGTAGTAACTGTAAGAAAAAGCCCTGGAGTGACCAAGTTGTGGCTACCCAGATTGAG	600
753	Db	TCCTGTAGTAACTGTAAGAAAAAGCCCTGGAGTGACCAAGTTGTGGCTACCCAGATTGAG	812
601	QY	AATGTTAAAGGCACTGAGGACTCAGGCACCAACAGTGTGTGGCCCTGGTCATTTCTTT	660
813	Db	AATGTTAAAGGCACTGAGGACTCAGGCACCAACAGTGTGTGGCCCTGGTCATTTCTTT	872
661	QY	GGTCTTTGGCCTTTATCCCTTCTTCATTGGTTTAAATGTATCGCTACCAACGGTGGAA	720
873	Db	GGTCTTTGGCCTTTATCCCTTCTTCATTGGTTTAAATGTATCGCTACCAACGGTGGAA	932
721	QY	TCCAAGCTCTACTCCATTTGTTTGGGAAATGCACACTGGAAGAGGGGGAGCTTGAA	780
933	Db	TCCAAGCTCTACTCCATTTGTTTGGGAAATGCACACTGGAAGAGGGGGAGCTTGAA	992
781	QY	GGAACTACTACTAAGCCCTGGCCCCAAACCCAAAGCTTCAGTCCCCTTCAGGCTTCACC	840
993	Db	GGAACTACTACTAAGCCCTGGCCCCAAACCCAAAGCTTCAGTCCCCTTCAGGCTTCACC	1052
841	QY	CCACCCCTGGGCTTCAGTCCCGTGCCAGTTCACACCTTCACCTCCAGCTCCACTATACC	900
1053	Db	CCACCCCTGGGCTTCAGTCCCGTGCCAGTTCACACCTTCACCTCCAGCTCCACTATACC	1112
901	QY	CCCGGTGACTGTCCCAACTTTTGGGGTCCCGCCAGAGAGGTGGCACACCCCTATCAGGG	960
1113	Db	CCCGGTGACTGTCCCAACTTTTGGGGTCCCGCCAGAGAGGTGGCACACCCCTATCAGGG	1172
961	QY	GCTGACCCCATCTTGGGACAGCCCTCGCCTCCGACCCCATCCCAACCCCTTCAGAAG	1020
1173	Db	GCTGACCCCATCTTGGGACAGCCCTCGCCTCCGACCCCATCCCAACCCCTTCAGAAG	1232
1021	QY	TGGGAGGACAGCGCCCAAGCCACAGAGCCTTAGACACTGATACCCCGCGAGCGCTGTAC	1080
1233	Db	TGGGAGGACAGCGCCCAAGCCACAGAGCCTTAGACACTGATACCCCGCGAGCGCTGTAC	1292
1081	QY	GCCTGTGTGAGAACGTGCCCGGTTGCGCTGGAAGGAATTC	1122
1293	Db	GCCTGTGTGAGAACGTGCCCGGTTGCGCTGGAAGGAATTC	1334

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2003, 01:14:14 ; Search time 81 Seconds
(without alignments)
1722.690 Million cell updates/sec

Title: US-09-899-422A-2

Perfect score: 2487
Sequence: 1 MGLSTVPDLLPLVLELLV.....DIEEALCPAALPPAPSLLR 455

Scoring table:
BLASUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame_p2n.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool/US09899422/runat_04062003.145737.14726/app_query.fasta_1.647
-DB=Issued Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPLC=0
-LOOPEXT=0 -UNIPS-bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09899422.ecgn_1.1.61.ernat_04062003.145737.14726 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents_NA:*
1: /cgn2.6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2.6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2.6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2.6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2.6/ptodata/1/ina/PTCUS_COMB.seq:*
6: /cgn2.6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2487	100.0	2161	3	US-09-106-038A-1
2	2487	100.0	2161	4	US-09-505-250-3
3	2487	100.0	2175	1	US-08-321-668-1
4	2487	100.0	2175	1	US-08-837-941-1
5	2487	100.0	2175	1	US-08-126-016-1
6	2487	100.0	2175	1	US-08-054-970-1
7	2482	99.8	2062	1	US-08-050-319B-24
8	2482	99.8	2062	2	US-08-465-982-24
9	1521	61.2	1956	2	US-08-762-308-10
10	1517	61.0	2440	1	US-09-513-007-1
11	1223.5	49.2	6889	1	US-08-286-740-2
12	1223.5	49.2	6889	5	PCR-US95-09576-2

13	1192	47.9	6896	2	US-08-627-151A-6	Sequence 6, Appl
14	1124	45.2	600	1	US-08-050-319B-47	Sequence 47, Appl
15	1124	45.2	600	1	US-08-465-982-47	Sequence 47, Appl
16	1016	40.9	1301	4	US-08-804-166-7	Sequence 7, Appl
17	1016	40.9	1301	4	US-08-910-991-7	Sequence 7, Appl
18	995.5	40.0	1147	4	US-08-804-166-5	Sequence 5, Appl
19	995.5	40.0	1147	4	US-08-910-991-5	Sequence 5, Appl
20	992	39.9	1478	4	US-09-149-922-6	Sequence 6, Appl
21	946	38.0	501	1	US-08-050-319B-1	Sequence 1, Appl
22	946	38.0	501	1	US-08-465-982-1	Sequence 1, Appl
23	946	38.0	504	1	US-08-050-319B-56	Sequence 56, Appl
24	946	38.0	504	2	US-08-465-982-56	Sequence 56, Appl
25	941	37.8	483	4	US-09-326-394-1	Sequence 1, Appl
26	870.5	35.0	1202	4	US-08-804-166-3	Sequence 3, Appl
27	870.5	35.0	1202	4	US-08-910-991-3	Sequence 3, Appl
28	854.5	34.4	477	2	US-08-050-319B-53	Sequence 53, Appl
29	854.5	34.4	477	2	US-08-465-982-53	Sequence 53, Appl
30	852	34.3	1049	4	US-08-804-166-1	Sequence 1, Appl
31	852	34.3	1049	4	US-08-910-991-1	Sequence 1, Appl
32	840	33.8	462	1	US-08-050-319B-51	Sequence 51, Appl
33	840	33.8	462	1	US-08-465-982-51	Sequence 51, Appl
34	840	33.8	474	1	US-08-050-319B-49	Sequence 49, Appl
35	840	33.8	474	2	US-08-465-982-49	Sequence 49, Appl
36	738.5	29.7	543	4	US-09-513-007-3	Sequence 3, Appl
37	731	29.4	372	1	US-08-050-319B-3	Sequence 3, Appl
38	731	29.4	372	2	US-08-465-982-3	Sequence 3, Appl
39	582	23.4	427	4	US-09-397-787-236	Sequence 236, App
40	395.5	15.9	1783	3	US-08-815-469-1	Sequence 1, Appl
41	387	15.6	1634	4	US-08-928-069-11	Sequence 11, Appl
42	387	15.6	1634	4	US-08-828-683A-9	Sequence 9, Appl
43	378	15.2	1254	3	US-08-815-469-3	Sequence 3, Appl
44	246	9.9	1600	3	US-08-602-791-1	Sequence 1, Appl
45	246	9.9	3386	4	US-09-041-886-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-106-038A-1
; Sequence 1, Application US/09106038A
; Patent No. 6007995
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker and Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Isis Pharmaceuticals, Inc.
; STREET: 2292 Faraday Avenue
; CITY: Carlsbad
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92008
; COMPUTER READABLE FORM:
; Sequence 1, 3.5 inch disk, 1.44 Mb
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,038A
; FILING DATE: June 26, 1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Laurel Spear Bernstein
; REGISTRATION NUMBER: 37,280
; REFERENCE/DOCKET NUMBER: RTS-0004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (760) 931-9200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2161
; TYPE: nucleic acid

Qy	1	MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuLeuVal	20
Db	256	ATGGGCTCTCCACCGTGCTGACCTGCTCTGCCCTGGTGTCTCTGGAGCTGTGTGGTG	315
Qy	21	GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg	40
Db	316	GGAAATATACCCCTCAGGGGTATTGGACTGTGTCCTCACCCTAGGGGACAGGAGAGAGA	375

QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
DB 376 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCCAAAATAATTCGATTTCGTGTACC 435
QY 61 LysCysHisLysGlyThrTyrIleTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
DB 436 AAGTCCCAAGAAAGAACTACTTGTACAACTGACTTCCAGGCCCGGGCAGGATACGGAC 495
QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
DB 496 TGCAGGAGTGTGAGAGCGCTCCTTCCACCGCTTCAGAAACACCTCAGACACTGCCTC 555
QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
DB 556 AGCTCTCCAATGCGAAGAAATGGTGCAGTGGAGATCTCTTCTTGCACAGTGGAC 615
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
DB 616 CGGGACACCGTGTGGCTGCAGGAAGAACCAAGTACCGCATATTGGAGTGAACCTT 675
QY 141 PheGlnCysPheAsnSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
DB 676 TTCCAGTCTCAATTGAGCTCTGCTCAATGGACCGTGCACCTCTCTCTGCCAGAG 735
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
DB 736 AAACAGAACACCGTGCACCTGCCATGCCATGCAGGTTCTTTCTAAGAGAAACAGTGTGTC 795
QY 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
DB 796 TCCCTAGTAACGTAAAGAAAGCCTGGAGTGCAGCAAGTGTGCTACCCCGAGATTGAG 855
QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
DB 856 AATGTTAAGGACACTGAGGACTCAGCACCAAGCTGTGTCCTGTGTCATTTTCITT 915
QY 221 GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
DB 916 GGTCTTTGCTTTTATCCTCTCTCTCATTTGTTTAAATGTATCGTACCAACGGTGGAG 975
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeuLeuGlu 260
DB 976 FCCAAGCTCTACTCCTGTTGTGGAAATCCACACCTGAAAGAGGGGAGCTTGA 1035
QY 261 GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
DB 1036 GGAACCTACTAAGCCCTGCGCCCAACCAAGCTTCAGTCCCACTCCAGGCTTCA 1095
QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrThr 300
DB 1096 CCCACCTGGGCTTCAGTCCGCTGCGCAGTTCCACCTTCACCTCCAGCTCCACCTATACC 1155
QY 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProThrGlnGly 320
DB 1156 CCGGTGACTGTCCCAACTTCCGCTCCCGCAGAGGTGGCCACCCCTATCAGGG 1215
QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
DB 1216 GCTGACCCCATCTTCCGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1275
QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
DB 1276 TGGAGGAGCAGCGCCCAAGCCACAGAGCTTAGACACTGATGACCCCGCAGCTGTAC 1335
QY 361 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu 380
DB 1336 GCGGTGGTGAAGACGTGCCCCGTGCGCTGGAAGAAATTCGTGCGCGCTAGGGCTG 1395
QY 381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
DB 1396 ACGGACACAGATCATCGGTGGAGCTGCAGACCGGCGCTGCTGCGCGAGGCGCAA 1455

QY 401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
DB 1456 TACAGCATGTGCGACCTGGAGGGGGGCGACCGCGCGCGGAGCCACGCTGGAGCTG 1515
QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
DB 1516 CTGGGACGGTGTCTCCGGACATGACCTGCTGGCTGGCTGGAGGACATCAGGAGGG 1575
QY 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
DB 1576 CTTTGGCGCGCGCGCGCTCCCGCGCGCGCGCTTCTCTCAGA 1620

RESULT 3

US-08-321-668-1
; Sequence 1, Application US/08321668
; Patent No. 5665859

GENERAL INFORMATION:

APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARPOLOMEEV, Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/321,668
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 256...1620
US-08-321-668-1

Alignment Scores:

Pred. No.: 3 12e-229 Length: 2175
Score: 2487.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-899-422A-2 (1-455) x US-08-321-668-1 (1-2175)

QY	1	MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuGluLeuVal	20
Db	256	ATGGCGCTCCACCGTGCCTGACTCCTGCCGTGGTGCTCCTGGAGCTGTGGTG	315
QY	21	GlyIleTyPProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg	40
Db	316	GGAAATAACCCCTCAGGGGTTATTGGACTGGTCCTCACCTAGGGGACAGGGAGAAGA	375
QY	41	AspSerValCysProGlnGlyLysTryIleHisProGlnAAsnAsnSerIleCysCysThr	60
Db	376	GATAGTGTGTCCCCAAGAAAAATATATCCACCCTCAAATAATTCGATTTCGTACC	435
QY	61	LysCysHisLysGlyThrTyRLeuTyRAsnAsPCysProGlyProGlyGlnAspThrAsp	80
Db	436	AAGTGCACAAAAGAACTACTTGTACAATGACTGCCAGGCCGGGGCAGGATACGGAC	495
QY	81	CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu	100
Db	496	TGCAGGAGTGTGAGAGCGCTCCTTACCGCTTCAGAAACCACTTCAGACACTGCCTC	555
QY	101	SerCysSerLysCysArgLysGluMetGlyGlnValIleLysSerSerCysThrValAsp	120
Db	556	AGCTGTCCAAATGCCAAGAAAGTAATGGGTCCAGTGGAGATCTCTTTCGCACAGTGGAC	615
QY	121	ArgAspThrValCysGlyCysArgLysAsnGlnTyRArgHisTyRTrpSerGluAsnLeu	140
Db	616	CGGGACACCGTGTGGCTCAGAGAAACCACTACCGCATTTATTTGGAGTAAAAACCTT	675
QY	141	PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu	160
Db	676	TTCCAGTGCCTCAATTCACGCTCGCTCAATGGGACCGTGCACTCTCTCTGCCAGGAG	735
QY	161	LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal	180
Db	736	AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTTCTTTCTAAGAGAAAAACGAGTGTCT	795
QY	181	SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu	200
Db	796	TCCTGTAGTAACGTGAAGAAACCGTGGAGTGACCAAGTTGTGGCTACCCCAGATTGAG	855
QY	201	AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe	220
Db	856	AATGTTAAGGGCACTCAGGACTCAGGACCCACAGTGTGTGTGCCCTTGGTCATTTCTTTT	915
QY	221	GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyRArgTyRGlnArgTriPLys	240
Db	916	GGTCTTTGCCTTTTATCCCTCCCTCATTTGGTTTTAATGTATCGCTACCAACCGTGAAG	975
QY	241	SerLysLeuTyRSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu	260
Db	976	TCCAAGCTCTACTCCATTTGTTGGGAATTCACACCTGAAAAAGAGGGGGAGCTTGA	1035
QY	261	GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr	280
Db	1036	GGAACTACTACTAAGCCCCCTGGCCCCAAACCCAAAGCTTCAGTCCCCACTCCAGGCTTCACC	1095
QY	281	ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyRThr	300
Db	1096	CCCACCTGGGCTTCAGTCCCGTGCCAGTTCACCTTCACCTCCAGCTCCACCTATACC	1155
QY	301	ProGlyAspCysProAsnPheAlaIalaProArgArgGluValAlaProProTyRGlnGly	320
Db	1156	CCSGGGTAGTGTCCCAACTTTGGGGTCCCGCAGAGAGGTGGCACCACTATCAGGG	1215

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 256..1620
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 319..1620
US-08-126-016-1

Alignment Scores:

Pred. No.: 3,12e-229 Length: 2175
Score: 2487.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-899-422a-2 (1-455) x US-08-126-016-1 (1-2175)

Oy 1 MetGlyLeuSerThrValProAspLeuLeuValLeuLeuVal 20
Db 256 ATGGGCTCTCCACGGTCCCTGACTGCTGCTGCGGCTGGTCTCTGGAGCTGTGGTG 315
Oy 21 GlyTleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluYsArg 40
Db 316 GGAATATACCCCTCAGGGGTTATTGGACTGTGCTCCTCACCTAGGGGACAGGAGAGA 375
Oy 41 AspSerValCysProGlnGlyTyrIleHisProGlnAsnAnSerIleCysCysThr 60
Db 376 GATAGTGTGTGTCGCCAAGGAATATATCCACCTCAAAATAATTCGATTTGCTGTACC 435
Oy 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
Db 436 AAGTGCCACAAAGGAACCTACTTACAAATGACTGTCCAGGCCCGGGCAGGATACGGAC 495
Oy 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db 496 TGCAGGAGTGTGAGAGCGGCTCTTCCACGCTTCAGAAACACCACTCAGACACTGCGTC 555
Oy 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db 556 AGCTGCTCCAAATCCCAAGGAATGGTCAAGTGGAGATCTCTTCTTGACAGCTGGAC 615
Oy 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
Db 616 CGGACACCGTGTGGCTGCAGGAAGAACCAAGTACCGGCAATATTGGAGTGAACCTT 675
Oy 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 676 TTCCAGTGTCTCAATTGACGCTGTGCTCAATGGGACCGTGCACCTCTCTCTGCCAGGAG 735
Oy 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db 736 AACAGAACACCGTGTGCACCTGCATGCAGGTTCTTCTTAAGAGAAACAGAGTGTCTC 795
Oy 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 796 TCCGTAGTAACTGTAAGAAAGCGTGGAGTGCACGAAGTGTGCTACCCACCCAGATTGAG 855
Oy 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
Db 856 AATGTTAAGGCACTGAGGACTAGGACCACTAGGACCACTAGTGTGTGCGGCTGGTCATTTCT 915
Oy 221 GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTyrLys 240
Db 916 GGTCTTTGGCTTTATCCCTCTCTTCATTTGGTTATATGATATCGTACCAACGGTGAAG 975
Oy 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeuGlu 260
Db 976 TCCAAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 1035

Oy 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 1036 GGAAGTACTACTAAGCCCTTGGCCCCAAACCAAGCTTCACTCCACTCCAGGCTTACC 1095
Oy 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrThr 300
Db 1096 CCCACCTGGGCTTCACTGCCGCTGCCAGTTCCACCTTCACTCCAGCTCCACCTATACC 1155
Oy 301 ProGlyAspCysProAsnProAlaProArgGluValAlaProProTyrGlnGly 320
Db 1156 CCCGCTGACTGTCCCACTTTGCGGCTCCCGCAGAGAGGTGGCCACCTATCAGGG 1215
Oy 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnIys 340
Db 1216 GCTGACCCCTCTTTCGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAAGAG 1275
Oy 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
Db 1276 TGGAGGACAGCGGCCCAAGCCACAGAGCTAGACACTGATGACCCCGGACGCTGTAC 1335
Oy 361 AlaValValGluAsnValProProLeuArgTyrLysGluPheValArgLeuGlyLeu 380
Db 1336 GCCGTGTGGAGAACGTGCCCGCTTGGCTGGAGGAAATTCGTCCGCGGCTTAGGCTG 1395
Oy 381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
Db 1396 AGCAGCACAGATCGATCGCTGGAGTGCAGAACGGCGCTGCTGCGGAGGCGCAA 1455
Oy 401 TyrSerMetLeuAlaThrTyrAspArgArgThrProArgArgGluAlaThrLeuGluLeu 420
Db 1456 TACAGCATGTGGCGACCTGGAGCGCGCACCGCGCGGCGGAGGCGGACGCTGAGCTG 1515
Oy 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla 440
Db 1516 CTGGAGCGCTGCTCCGAGCATGGACCTGCTGGGCTGCTGGAGGACATCGAGAGCGG 1575
Oy 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
Db 1576 CTTTGGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1620

RESULT 6

US-08-054-970-1
; Sequence 1, Application US/08054970
; Patent No. 6395267
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; TITLE OF INVENTION: TNF RECEPTOR ACTION MODULATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/054,970
; FILING DATE: 03-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2175 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 256..1620

; US-08-054-970-1

Alignment Scores:

Pred. No.: 3,12e-229 Length: 2175

Score: 2487.00 Matches: 455

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-09-899-422A-2 (1-455) x US-08-054-970-1 (1-2175)

```

QY      1 MetGlyLeuSerThrValProAspLeuLeuValLeuLeuValLeuVal 20
DB      |||||||
QY      21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
DB      |||||||
QY      316 GGAATATACCCCTCAGGGGTTATTGGACTGTGTCCCTCACCTAGGGGACAGGAGAGAGA 375
DB      |||||||
QY      41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
DB      |||||||
QY      376 GATAGTGTGTGCCCAAGGAAATATATCCACCTCCAAATTAATTCGATTTCGTGTACC 435
DB      |||||||
QY      61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
DB      |||||||
QY      436 AAGTCCCAACAAGAACCTACTTGTACATGACTGTCCAGGCCCGGGGACGATACGGAC 495
DB      |||||||
QY      81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
DB      |||||||
QY      496 TGCAGGGAGTGTGAGAGCGGCTTCCTTCACCGCTTCAGAAACACCTCAGACACTGCCTC 555
DB      |||||||
QY      101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
DB      |||||||
QY      556 AGCTGCTCAAATGCGGAAGAAATGGCTCAGGTGGAGATCTCTTTCACACTGGAC 615
DB      |||||||
QY      121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
DB      |||||||
QY      616 CGGGACACCGTGTGTGGCTGCAGGAAGAACCACTACCGGCATATTGGAGTGAACACTT 675
DB      |||||||
QY      141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
DB      |||||||
QY      676 TTCCAGTGCTTCAATTGACGCTCTGCTCAATGGACCGTGCACCTCTCTCTGCCAGGAG 735
DB      |||||||
QY      161 LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysVal 180
DB      |||||||
QY      736 AAACAGAACCCGTGTGCACCTGCCATGCAGGTTTCTTCTAAGAAACACGAGTGTGTC 795
DB      |||||||
QY      181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
DB      |||||||
QY      796 TCCTGTAGTAACTGTGAAGAAACCTGGAGTGCACGAGTGTGCTACCCAGATGTAG 855
DB      |||||||
QY      201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
DB      |||||||
QY      856 AATGTTAAGGCACTGAGGACTCAGGCACACAGTGTCTGTGCCCTGTCATTTCTTT 915
DB      |||||||
QY      221 GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
DB      |||||||
QY      916 GGTCTTTGCTTTTATCCCTCTCTCAFTGTTTAAATGATATCGTACCAACGGTGGAG 975
DB      |||||||
QY      241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGluLeuGlu 260
DB      |||||||
QY      976 TCCAGCTCTACTCCATTGTTGTGGGAATCGACACCTGAAAGAGGGGAGCTTGAA 1035
DB      |||||||

```

```

QY      261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
DB      |||||||
QY      1036 GGAACCTACTACTAAGCCCTGCGCCCAACCAAGCTTCAGTCCACTCCAGGCTTCACC 1095
DB      |||||||
QY      281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrThr 300
DB      |||||||
QY      1096 CCCACCTGGGCTTCAGTCCCTGCGCCAGTTCACCTTCACCTCCAGCTCCACCTATACC 1155
DB      |||||||
QY      301 ProGlyAspCysProAsnPheAlaAlaProArgGluValAlaProProThrGlnGly 320
DB      |||||||
QY      1156 CCGGTGACTGTCCCAACTTTCGGGCTCCCGCAGAGAGTGGCACCACCTATCAGGGG 1215
DB      |||||||
QY      321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
DB      |||||||
QY      1216 GCTGACCCCATCTTCGACAGACCTCGCTCGACCCCATCCCAACCCCTTCAGAAG 1275
DB      |||||||
QY      341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
DB      |||||||
QY      1276 TGGGAGGACAGCGCCCAAGCCACAGACCTAGACACTGATGACCCCGCAGCTGTAC 1335
DB      |||||||
QY      361 AlaValValGluAsnValProProLeuArgTyrTrpLysGluPheValArgLeuGlyLeu 380
DB      |||||||
QY      1336 GCGGTGGTGAGAACGTGCCCTTCCTGGAAGGAATTCGTGGGCGCCTTAGGGCTG 1395
DB      |||||||
QY      381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
DB      |||||||
QY      1396 AGCGACACAGAGATCGATCGGTGGAGTGCAGACGGGCGCTGCCTGCGCGAGGCGCAA 1455
DB      |||||||
QY      401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
DB      |||||||
QY      1456 TACAGCATCTGGCGACCTGGAGGGGCGCACGCCGCGCGAGGCCACGCTGGAGCTG 1515
DB      |||||||
QY      421 LeuGlyArgValLeuArgAspMetAspLeuGlyCysLeuGluAspIleGluAla 440
DB      |||||||
QY      1516 CTGGGACGGTGTCTCGCGACATGACCTGTGGGCTGCTGGAGACATCGAGGAGGCG 1575
DB      |||||||
QY      441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
DB      |||||||
QY      1576 CTTTGGGCGCGCGCCCTCCCGCGCGCGCGAGTCTTCTCAGA 1620
DB      |||||||

```

RESULT 7

US-08-050-319B-24

; Sequence 24, Application US/08050319B

; Patent No. 5633145

; GENERAL INFORMATION:

; APPLICANT: M.Feldmann, P.W. Gray,

; APPLICANT: M.J.C. Turner, F.M. Brennan

; TITLE OF INVENTION: Modified human TNFalpha (Tumor

; TITLE OF INVENTION: Necrosis Factor alpha) Receptor

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Reed & Robbins

; STREET: 635 Bryant Street

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/050,319B

; FILING DATE: 10-May-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Robbins, Roberta L.

; REGISTRATION NUMBER: 33,208

; REFERENCE/DOCKET NUMBER: 5150-0030

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 617-8999


```

; ; REGISTRATION NUMBER: 33,208
; ; REFERENCE/DOCKET NUMBER: 5150-0030
; ;
; ; TELECOMMUNICATION INFORMATION:
; ;
; ; TELEPHONE: (415) 617-8999
; ;
; ; TELEFAX: (415) 327-3231
; ;
; ; INFORMATION FOR SEQ ID NO: 24:
; ;
; ; SEQUENCE CHARACTERISTICS:
; ;
; ; LENGTH: 2062 base pairs
; ;
; ; TYPE: nucleic acid
; ;
; ; STRANDEDNESS: double
; ;
; ; TOPOLOGY: linear
; ;
; ; MOLECULE TYPE: cDNA to mRNA
; ;
; ; FEATURE:
; ;
; ; NAME/KEY: CDS
; ;
; ; LOCATION: 155..1519
; ;
; ; US-08-465-982-24

```


STRANDEDNESS: double
TOPOLOGY: linear
US-08-286-740-2

Alignment Scores:

Pred. No.: 5.27e-107 Length: 6889
Score: 1223.50 Matches: 257
Percent Similarity: 64.04% Conservative: 19
Best Local Similarity: 59.63% Mismatches: 61
Query Match: 49.20% Indels: 95
DB: 1 Gaps: 11

US-09-899-422a-2 (1-455) x US-08-286-740-2 (1-6889)

```

Qy 1 MetGlyLeuSerThrValProAspLeuLeuValLeuLeuValLeuVal 20
Db 1605 ATGGGCTCTCCACCGTGCCTGCTGCTGCGGTGGTCTCTGGAGCTGTGGTG 1664
Qy 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
Db 1665 GGAATATACCCCTCAGGGGGTATTGGACTGGTCCCTCACCTAGGGGACAGGAGAAGA 1724
Qy 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
Db 1725 GATAGTGTGTGTCCTCCAGGAAATATATCCCTCCAAATAATTGATTTGCTGTACC 1784
Qy 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
Db 1785 AAGTGCACAAAGCAACTACTTGTACAAATGACTGTCCAGGCCGGGACGATACGGAC 1844
Qy 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db 1845 TGCAGGAGGTGTGAGACGGCTCTTCCACCGCTTCAGAAAACCACTCAGACACTGCTC 1904
Qy 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db 1905 AGCTGCTCCAAATGCCAAGGAATATGGTCAAGTGGAGATCTCTTCTGCACAGTGGAC 1964
Qy 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisLysTyrSerGluAsnLeu 140
Db 1965 CGGACACCGTGTGGCTGTCAGGAAGAACCACTACCGGCAATATTGGAGTGAACCTT 2024
Qy 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 2025 TTCCAGTGTCTCAATTCAGCGCTGCTCAATGGGACCGTGCACCTCTCTCTGCCAGGAG 2084
Qy 161 LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysVal 180
Db 2085 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTCTTCTTAAGAGAAACAGAGTGTGC 2144
Qy 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 2145 TCCTGTAGTAACGTGAAGAAAGCTGGAGTGCACGAAGTGTGCTTACCCACAGATTGAG 2204
Qy 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
Db 2205 AATGTTAAGGCACTGAGGACTCAGGCACCACA----- 2237
Qy 221 GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTyrLys 240
Db 2237 ----- 2237
Qy 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeu---- 259
Db 2238 -----GACAAGAGAGTTGACCTCAAA 2258
Qy 260 -----GluGlyThrThrThrLysProLeuAlaProAsnProSerPheSerPro 275
Db 2259 ACCCCACTTGGTACACAACTACACATGCCCGGTGCCAGACGCCCAAACTCTGTGAC 2318
Qy 276 ThrProGlyPheThrProThrLeuGlyPheSerProValProSerSerThrPheThrSer 295
Db 2319 ACACCT-----CCCCGGTCCCGTGCACGAGCCC----- 2351

```

```

Qy 296 SerSerThrTyrThrProGlyAspCysProAsnPheAlaAlaProArgArg---GluVal 314
Db 2352 AAATCTTGTGACACACACCTCCCCCATGCCAGGTGCCAGAGCCCAATCTTGTGACACA 2411
Qy 315 AlaProPro-TyrGlnGlyAlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIle 334
Db 2412 CCTCCCCCATGCCAGGTGCC----- 2433
Qy 334 eProAsnProLeuGlnLysTyrGluAsp-----SerAlaHisLysProGlnSer----- 350
Db 2434 ----CAGCACCTGAACCTCTGGGAGGACCGTCACTCTCTCTCCCCCCCAAAACCCCAAG 2489
Qy 351 ----LeuAspThrAspAspProAlaThrLeuTyrAlaValValGluAsnVal----- 366
Db 2490 GATACCTTATGATTTCCCGGACCCCT--GAGGTCACTGCGTGGTGGTGGAGCGGACCA 2548
Qy 367 ----ProProLeuArgTyrLysGluPheValArgLeuGlyLeuSerAspHisGlu 384
Db 2549 CGAAGACCCCGAGGTGCCAGTTCAGTTCAGTGTG----- 2582
Qy 384 uIleAspArgLeuGlnLeuGlnAsnGlyArgCysLeu---ArgGluAlaGlnTyrSerMe 403
Db 2583 ----GACGGCTGGAGGTGCATATGCCAAGACAAAGCCGGGAGGAGGAGGAGTTCACACAG 2638
Qy 403 tLeu-AlaThrTyrArgArgThrPro 412
Db 2639 CACGTTCGGTGTGTCGACGCTCCTCACGG 2667

```

RESULT 12

PCT-US95-09576-2
: Sequence 2, Application PC/TUS9509576
: GENERAL INFORMATION:
: APPLICANT: GENENTECH, INC.
: TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
: TITLE OF INVENTION: HOST CELLS
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/09576
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/286740
: FILING DATE: 05-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 00,000
: REFERENCE/DOCKET NUMBER: 798PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6889 bases
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
PCT-US95-09576-2

Alignment Scores:

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2003, 00:13:39 ; Search time 2999 Seconds
(without alignments)
4415.397 Million cell updates/sec

Title: us-09-899-422a-2

Perfect score: 2487

Sequence: 1 MGLSTVPDLLPLVLELLV.....DIEEALCGPALPPAPSLLR 455

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL-frame+p2n.model -DEV-rlp
-Q/cgn2_1/USPTO_spool/US09899422/runat_04062003_145736_14704/app.query.fasta_1.647
-DB-GenEmbl -QFMT-fastp -SUFFIX-rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=ptc -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09899422.ecgn_1_1_3745_erunat_04062003_145736_14704 -NCPU=6 -ICPU=3
-NO_JMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.ph:*
24: em.pl:*
25: em.ro:*
26: em.sts:*
28: em.un:*

29: em.vi:*
30: em.htg_hum:*
31: em.htg_inv:*
32: em.htg_other:*
33: em.htg_mus:*
34: em.htg_pln:*
35: em.htg_rod:*
36: em.htg_man:*
37: em.htg_vrt:*
38: em.sy:*
39: em.htgo_hum:*
40: em.htgo_mus:*
41: em.htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2487	100.0	1368	6	A29098
2	2487	100.0	2062	6	A21522
3	2487	100.0	2087	9	HUMTNFR
4	2487	100.0	2111	6	A26412
5	2487	100.0	2111	6	AX409713
6	2487	100.0	2111	9	HUMTNFRB
7	2487	100.0	2112	9	HUMTNFRC
8	2487	100.0	2161	6	AR096330
9	2487	100.0	2161	9	HSTNFR1A
10	2487	100.0	2175	6	A43873
11	2487	100.0	2175	6	A78738
12	2487	100.0	2175	6	AR041076
13	2487	100.0	2175	6	I64751
14	2487	100.0	2176	6	AI9907
15	2487	100.0	2194	9	BC010140
16	2482	99.8	2062	6	I43805
17	2471	99.4	2109	9	AK056611
18	2460	98.9	2061	6	A20255
19	2444	98.3	2050	9	HUMTNFRP
20	2053.5	82.6	1331	6	A29103
21	1801.5	72.4	2171	4	AB051103
22	1738	69.9	2004	4	SSU19994
23	1670	67.1	17350	9	AY131997
24	1670	67.1	188488	9	AC006057
25	1563.5	62.9	2115	10	AF329976
26	1563.5	62.9	2130	6	AX401925
27	1563.5	62.9	2130	10	RAFTNFR
28	1560.5	62.7	2115	10	AF329977
29	1559.5	62.7	2115	10	AF329978
30	1559.5	62.7	2115	10	AF329979
31	1559.5	62.7	2115	10	AF329980
32	1559.5	62.7	2115	10	AF329981
33	1521	61.2	1956	10	MUSTNFR2
34	1521	61.2	2048	10	MMP55R
35	1521	61.2	2063	10	MUSTNFR1
36	1521	61.2	2086	10	BC004599
37	1521	61.2	2154	10	MUSTNFX
38	1521	61.2	2179	10	MMTNFR5
39	1517	61.0	2440	4	BTU90937
40	1223.5	49.2	6889	6	I26928
41	1213.5	48.8	2254	9	HUMTNFR103
42	1192	47.9	6896	6	AR031375
43	1192	47.9	6896	6	BD009743
44	1130	45.4	600	6	A20257
45	1124	45.2	600	6	I43808

ALIGNMENTS

RESULT 1

POGKVIHPQNNISICTCKHGTLYLNDPCPGQDNDRECSGSGSTASENHLRHCLSC
SKCRKMGVEISSCTVDRTVCGCRKNQYRHYNSENLFCQFNCSLCINGTVHLSCQE
KONTVCCHAGFFLENECVSCNCKSLECKLQIPOIENVKGTEDSGTVLLPLVI
PFGCLLSLITGLMYRQWKSLSYVCGKSTPEKEGELEGTTRKPLANPSFPT
PGFTPLGFSVPVSTFTSSSTYTPGDCPNRAAPREVAIPPYOGADPILANALASDPI
PNPLOKWDASHKQSLDTPDAPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLQON
PRLKREAGYSMLAYWRRTPREATLELGRVLRDMDLJGCLLEIEALCGPAALPPA
PSLLR

BASE COUNT 433 a 624 c 591 g 449 t

Alignment Scores:

Pred. No.: 2,85e-154 Length: 2087
Score: 2487.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-899-422A-2 (1-455) x HUMTNPFR (1-2087)

QY 1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuLeuVal 20
DB 182 ATGGGCGCTCCACCGTGCCTGACCTGCTGCTGCGCGCTGGTCTCTCGAGCTGTGGTG 241
QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGlnLysArg 40
DB 242 GGAATATACCCCTCAGGGGGTATTGGACTGTGCTCCCTACCTAGGGGACAGGAGAGA 301
QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
DB 302 GATAGTGTGTGCCAGGAGAAATATATCCACCTCAAAATAATTCGATTGTGTATCC 361
QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
DB 362 AAGTCCCAAGGAACCTACTTGTACAAATGACTGTCCAGCGCCGGGCGAGATACGCAC 421
QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
DB 422 TGCAGGGAGTGTGAGAGCGGTCTTCCCGCTTCAGAAACCAACCACTCAGACACTGCGTC 481
QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
DB 482 AGCTGCTCCAATGCCAGAAAGAAATGGTCAAGTGGAGATCTCTTCTTGCACAGTGAC 541
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
DB 542 CGGGACACCGTGTGTGGCTGCAGGAAGAACCACTACCGGCATTTATGGAGTGAACACCTT 601
QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
DB 602 TTCAGTGTCTCAATTTGAGCCTCTGCTCAATGGGACCGTGCACCTCTCTCTGCCAGGAG 661
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
DB 662 AAACAGAACACCGTGTGCACCTGCCATGCAGTTCCTTCTTCAAGAAACAGTGTGTC 721
QY 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
DB 722 TCCTGTAGTAACCTTAAGAAAGACCTGGAGTGCAGGAAGTGTGCTTACCCACAGATTGAG 781
QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
DB 782 AATGTTAAGGGCATGTAGGACTCAGGCACACAGTGTGTTGGCCCTGTGCTATTTCTTT 841
QY 221 GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
DB 842 GGTCTTTGCCCTTTATCCCTCTCTTCAATGGTTAATGATATCGCTACCAACAGTGGAG 901
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeuGlu 260
DB 902 TCCAAGCTCTACTCCATTGTTGTGGGAAATCGACACCTGAAAGAGAGGGGAGCTTCAA 961

QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
DB 962 GGAACCTACTACTAAGCCCTTGCCCCCAACCAAGCTTCAGTCCACCTCCAGGCTTACC 1021
QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300
DB 1022 CCCACCCCTGGGCTTCAGTCCCGTGCCCGTTCACCTTCACCTCCAGCTCCACCTATACC 1081
QY 301 ProGlyAspCysProAsnPheAlaProArgArgGluValAlaProProTyrGlnGly 320
DB 1082 CCCGGTGACTGTCCCACTTTCGGGCTCCCCGACAGAGGTGGACACCTTCATCAGGG 1141
QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
DB 1142 GCTGACCCCATCTTTCGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAAG 1201
QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
DB 1202 TGGGAGGACAGCGCCCAAGCCACAGACCTAGACACTGATGACCCCGCAGCGTGTAC 1261
QY 361 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu 380
DB 1262 GCCGTGGTGGAGAGCTGCCCGCTTGGCTGGAGGAATTCGTCCGGCGCTAGGGGTG 1321
QY 381 SerAspHisGluIleAspArgLeuLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
DB 1322 AGCGACACAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCTCGCGAGCGCAA 1381
QY 401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
DB 1382 TACAGCATGCTGGCGACCTGGAGCGCGCGCACCGCGCGCGAGCCACCGTGGAGGTG 1441
QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
DB 1442 CTGGGACGCTGCTCCGCGACATGACCTGCTGGGCTGCCTGGAGGACATCGAGGAGCG 1501
QY 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
DB 1502 CTTTGGCGCGCGCGCTCCCGCGCGCGCGCTCTCTCAGA 1546

RESULT 4

LOCUS A26412 2111 bp DNA linear PAT 26-APR-1995
DEFINITION cDNA for (55KD TNF-BP) tumor necrosis factor binding protein from
patent EP0417563.
ACCESSION A26412
VERSION A26412.1 GI:904968
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 2111)
AUTHORS Brockhaus, M., Dembic, Z., Gentz, R., Lesslauer, W., Loetscher, H. and
Schlager, E.J.
TITLE TNF-binding proteins
JOURNAL Patent: EP 0417563-A 24 20-MAR-1991;
F. HOFFMANN-LA ROCHE AG
FEATURES
source
1. 2111
/organism="synthetic construct"
/db_xref="taxon:32630"
187..1554
/codon_start=1
/transl_table=11
/product="55 kD TNF-BP"
/protein_id="CAA01805.1"
/db_xref="GI:904968"
/translation="MGLSTVDPDLLLPLVLLLELVGIVPSGVIGLVPHLGDREKRSVC
POGKVIHPQNNISICTCKHGTLYLNDPCPGQDNDRECSGSGSTASENHLRHCLSC
SKCRKMGVEISSCTVDRTVCGCRKNQYRHYNSENLFCQFNCSLCINGTVHLSCQE
KONTVCCHAGFFLENECVSCNCKSLECKLQIPOIENVKGTEDSGTVLLPLVI
PFGCLLSLITGLMYRQWKSLSYVCGKSTPEKEGELEGTTRKPLANPSFPT
PGFTPLGFSVPVSTFTSSSTYTPGDCPNRAAPREVAIPPYOGADPILANALASDPI
PNPLOKWDASHKQSLDTPDAPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLQON
PRLKREAGYSMLAYWRRTPREATLELGRVLRDMDLJGCLLEIEALCGPAALPPA
PSLLR"
CDS

QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
 DB 247 GGAATATACCCCTCAGGGTTATTGGACTGTGTCCTCACCTAGGGACAGGAGAGA 306
 QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
 DB 307 GATAGTGTGTGTCACAGGAATAATATATCCACCTCAAAATAATTCGATTTCGTAC 366
 QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
 DB 367 AAGTGCCACAAGGAACCTACTTGTACATGACTTCCAGGCCCGGGCAGATACGGAC 426
 QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
 DB 427 TGCAGGGAGTGTGAGAGGGCTTCCTTCACCGCTTCAGAAACACCTCAGACACTGCCTC 486
 QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
 DB 487 ACCTGCTCCAAATGCGAAGGAATGGGTACGGTGGAGATCTCTTTCACAGTGGAC 546
 QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
 DB 547 CGGGACACCGTGTGTGCTGCAGGAAGAACACAGTACCGGCATTATTGGAGTGAACCTT 606
 QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
 DB 607 TTCCAGTGTCTCAATTCAGCCCTCTCCCTCAATGGGACCGTGCACCTCTCTGCCAGG 666
 QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
 DB 667 AAACAGAACCGTGTGCACCTGCCATCGCCTGAGGTTCTTTCTAAGAGAAACAGTGTGTC 726
 QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
 DB 727 TCCTGTAGTAACTGTAGAAAGCCTGGAGTGCACAGTGTGCTACCCACAGATTGAG 786
 QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
 DB 787 AATGTTAAGGGACACTGAGGACTCAGGCACACAGTGTGCTGCCCTGCTCATTTTCTTT 846
 QY 221 GlyLeuCysLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
 DB 847 GGTCTTTGGCTTTATCCCTCTCTCATGTTGTTATGTATCGCTACCAAGGTGGAG 906
 QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeuGlu 260
 DB 907 TCCAAAGCTACTCTCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTCAA 966
 QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
 DB 967 GGAACCTACTAAGCCCTCGCCCCCAACCCAAAGCTTCAGTCCCACTCCAGGCTTCA 1026
 QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrThrThr 300
 DB 1027 CCCACCTTGGGCTTCAGTCCCGTGCAGTCCACCTTCACCTCCAGCTCCACCTATACC 1086
 QY 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 320
 DB 1087 CCCGGTGACTGTCCCAACTTTGGCGCTCCCGCAGAGAGTGGCACCCACCTATCAGGG 1146
 QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
 DB 1147 GCTGACCCCATCTTTCGACAGCCCTCGCCCTCCGACCCATCCCAACCCCTTCAGAG 1206
 QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
 DB 1207 TGGAGGACAGGCCCAAGCCACAGACCTAGACACTGATGACCCCGCAGCGCTGATC 1266
 QY 361 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu 380
 DB 1267 GCCGTGTGTGAGAACGTCGCCCGTGGCTGGAGGAATTCGTGCGCGCCTAGGGCTG 1326
 QY 381 SerAspHisGluIleAspArgLeuLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400

DB 1327 AGCGACACGAGATCGATCGCTGGAGCTGCAGAACGGCGCTGCTCGCGAGCGCAA 1386
 QY 401 TyrSerMetLeuAlaThrTyrArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
 DB 1387 TACAGCATGCTGGCGACCTGGAGCGCGGCACCGCGCGCGAGGCCACCGCTGGAGCTG 1446
 QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
 DB 1447 CTGGGACCGGTGCTCCGCGACATGGACCTGCTGGGCTGCCCTGGAGGACATCGAGAGCG 1506
 QY 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
 DB 1507 CTTTGGCGCGCGCGCTCGCGCGCGCGCGCTCTCTCAGA 1551

RESULT 6

HUMTNFRB
 LOCUS Homo sapiens tumor necrosis factor receptor mRNA, complete cds.
 DEFINITION M58286.1 M33480
 ACCESSION M58286.1 GI:339753
 VERSION tumor necrosis factor receptor.
 KEYWORDS Human cell line HL60, cDNA to mRNA.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 2111)
 AUTHORS Loetscher, H., Pan, Y.C., Lahm, H.W., Gentz, R., Brockhaus, M.,
 Tabuchi, H. and Lesslauer, W.
 TITLE Molecular cloning and expression of the human 55 kd tumor necrosis
 factor receptor
 JOURNAL Cell 61 (2), 351-359 (1990)
 MEDLINE 90235284
 PUBMED 2158862

FEATURES

Location/Qualifiers
 1..2111
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_line="HL60"
 1..2111
 /gene="TNF receptor"
 187..1554
 /gene="TNF receptor"
 /note="55 kDa"
 /codon_start=1
 /product="tumor necrosis factor receptor"
 /protein_id="AAA36753.1"
 /db_xref="GI:339754"
 /translation="MGLSTVPDLLLPLVLELVGIVPSGVIGLVPHGLDREKRDVSC
 PQKYIHPQNNISICTKHKGTLYNDPCPGQDTCRECSGSFTASENHLRHCLSC
 SKRKEMGOVEISGCTVDRDVTGCRKNQYRHYWSENLPQCFNGLCLNGVHLSCOE
 KONTVCYCHAGFFLRENECVSCNKKSLCTKLCPLQIENVKGTSDGTVLLPLVI
 FFGCLLSLLFGLMYRQWKSKLYSTVCCKSTPEKEGELEGTTTPLANPSPPT
 PGPTPTLGFSPVSPSTTSSSTTYPGDCPNPAPRRVAPPYQGADPLATATLASDPI
 PNPLOKEDSAHKPQSLDTPDPAIYAVVENVPPLRWKFEYRRLGSLDSHEIDRLLELQN
 GRCLREAYQSMLATRRRTTPREATLELLLRVLRDMLLGLCLEDIEEALCPAALPPA
 PSLLR"
 187..273
 /gene="TNF receptor"
 274..1551
 /gene="TNF receptor"
 /product="tumor necrosis factor receptor"

sig_peptide

187..273

mat_peptide

274..1551

BASE COUNT 445 a 629 c 587 g 450 t
 ORIGIN

Alignment Scores:

Pred. No.: 2,89e-154 Length: 2111
 Score: 2487.00 Matches: 455
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

Qy		1	MetGlyLeuSerThrValProAspLeuLeuProIeuValLeuLeuGluLeuVal	20
Db		187	ATGGGCCTCCACCGTGCCTGCTCCTCGCTGCTCCTGGAGCTGTGGTG	246
Qy		21	GlvIleYrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg	40
Db		247	GGAAATATACCCCTCAGGGGTTATTGGACTGGTCCTCACTAGGGACAGGGAGAAGA	306
Qy		41	AspSerValCysProGlnGlyLysTyriIleHisProGlnAsnAsnSerIleCysCysThr	60
Db		307	GATAGTGTGTGCCAAGGAAAATAATACCACCTCAAATAATTCGATTGCTGTACC	366
Qy		61	LysCysHisLysGlyThrTyrlLeuTyraSnAspCysProGlyProGlyGlnAspThrAsp	80
Db		367	AAGTGCACAAGAAAGAACCTACTTGTCAATGACTGTCCAGGCCGGGGCAGGATACGGAC	426
Qy		81	CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu	100
Db		427	TGCAGGGAGTGTGAGAGCGGCTCCTTCAACGCTTCAGAAAAACCACTCACACACTGCCTC	486
Qy		101	SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValasp	120
Db		487	AGCTGCTCCAATAATGCCGAAGAGAAATGGGTCAAGTGGAGATCTCTTCTTCACAGTGGAC	546
Qy		121	ArgAspThrValCysGlyCysArgLysAsnGlnTyraArgHisTyrrTpSerGluAsnLeu	140
Db		547	CGGGACACCGTGTGGCTCGAGGAAGAACCATGACCGGCATTAATYGGAGTGAACACCTT	606
Qy		141	PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu	160
Db		607	TTCCAGTGTCTCAATTGACGCTGTGCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG	666
Qy		161	LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal	180
Db		667	AAACAGAAACACCGTGCACCTGCATGCAAGTTCCTTCTAGAGAAAACGAGTGTGTC	726
Qy		181	SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu	200
Db		727	TCCTGTAGTAACCTAAGAAAAGCGCTGGAGTGCACGAAGTGTGTGCTTACCCAGATTGAG	786
Qy		201	AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe	220
Db		787	AATGTTAAGGCACTGAGGACTCAGGCACACACAGTGTGTGGCCCCGGTCATTTCTTT	846
Qy		221	GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyraArgTyriGlnArgTrpLys	240
Db		847	GGTCTTTGCCCTTTATCCCCTCTTTCATTGGTTTAATGTATCGCTACCAACGGTGGAG	906
Qy		241	SerLysLeuTyrserIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu	260
Db		907	TCCAAGCTCTACTCCATGTTGTGGGAAATCGACACCTGAAAAAGAGGGGAGCTTGAA	966
Qy		261	GlyThrThrThrLysProLeuAlaProAsnPheSerPheSerProThrProGlyPheThr	280
Db		967	GGAACTACTAAGCCCTTGCCCCCAACCCAAAGCTTCAGTCCCACCTCAGGGCTTACC	1026
Qy		281	ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrrThr	300
Db		1027	CCCACCTGGGCTTCAGTCCCGTGCACGCTTCCACCTTCACCTCCAGCTCCACCTATACC	1086
Qy		301	ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProTyrrGlnGly	320
Db		1087	CCCCGGTAGCTGCCCAACTTGGCGCTCCCGCAGAGAGGTGGCACCACCTATPCAGGGG	1146
Qy		321	AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnPProLeuGlnLys	340
Db		1147	GCTCACCCCATCCTTGGACAGCCCTCGCTCCGACCCCATCCCCCAACCCCTTCAGAAG	1206
Qy		341	TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlathrLeuTyrr	360
Db		1207	TGGGAGACAGCGCCCAACAGCCACAGAGCTTAGACACTGATACCCCGGACGCTGTAC	1266

```
Pred. No.: 2,89e-154 Length: 2112
Score: 2487.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-899-422A-2 (1-455) x HDMTNPFC (1-2112)

QY 1 MetGlyLeuSerThrValProAspLeuLeuValProLeuValLeuGluLeuVal 20
Db 207 ATGGGCGCTCCACCGTGCCTGACCTGCTGCTGCCACCTGGTGCTCTGGAGCTGTGGTG 266
QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
Db 267 GGAATATACCCCTCAGGGGTATTGGAGCTGGTCCCTCACCTAGGGACAGGGAGAAGA 326
QY 41 AspSerValCysProGlnCysLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
Db 327 GATAGTGTGTGCCCAAGGAATAATATCCACCTCAAAATAATTCGATTTCGTGTACC 386
QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlnAspThrAsp 80
Db 387 AAGTCCACAAAGGAACCTACTTGTACATGACTCTCCAGGCGCGGGCAGCATACGGAC 446
QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db 447 TGCAGGGAGTGTGAGAGCGGCTCTTCCACCGCTTCAGAAACACCTCAGACACTGCCTC 506
QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db 507 ACCTGCTCCAAATGCGGAAGCAATGGCTGAGTGGAGATCTCTTTCACAGCTGGAC 566
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
Db 567 CGGGACACCGTGTGGCTGCGAGGAAGAACAGTACCGGCATATTGGAGTGAACCTT 626
QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 627 TTCCAGTGTCTCAATGGAGCGCTCTGCTCAATGGAGCGGTGCACCTCTCTCGCAGGAG 686
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db 687 AAACAGACACCGTGTGACCTGCCATGCCAGTTCCTTCTTAAGAAACACAGTGTGTC 746
QY 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 747 TCCTGTAGTAACTGTAAAGAAAGCGCTGGAGTGCACGAAGTGTGCTACCCAGATTGAG 806
QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
Db 807 AATGTTAAGGGCAGCTGAGGAGCTCAGGCACACAGTGTGTGGCCCTGGTCAATTTCTTT 866
QY 221 GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
Db 867 GGTCTTTGCCCTTTATCCCTCTCTTCATTGGTTAATGTATCGTACCAAGGTGGAG 926
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeuGlu 260
Db 927 TCCAAAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGA 986
QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 987 GGAAGTACTACTAGCCCTCGGCCCAACCAAGCTTCAGTCCACCTCCAGGCTTACC 1046
QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrTyrThr 300
Db 1047 CCCACCTGGGCTTCAGTCCCGTGGCCAGTTCACCTTCACCTCCAGCTCCACCTATACC 1106
QY 301 ProGlyAspCysProAsnPhAlaAlaProArgArgGluValAlaProProTyrGlnGly 320
Db 1107 CCGGTGACTGTCCCAACTTTGCGGCTCCCGCAGAGAGGTGGCACCACCTATCAGGG 1166

LOCUS AR096330 2161 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 1 from patent US 6007995.
ACCESSION AR096330
VERSION AR096330.1 GI:10025045
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2161)
AUTHORS Baker,B.F. and Cowser,L.M.
TITLE Antisense inhibition of TNFR1 expression
JOURNAL Patent: US 6007995-A 1 28-DEC-1999;
FEATURES
source
location/Qualifiers
BASE COUNT 459 a 642 c 604 g 456 t
ORIGIN
Alignment Scores: 2,97e-154 Length: 2161
Pred. No.: 2487.00 Matches: 455
Score: 2487.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-09-899-422A-2 (1-455) x AR096330 (1-2161)

QY 1 MetGlyLeuSerThrValProAspLeuLeuValProLeuValLeuGluLeuVal 20
Db 256 ATGGGCGCTCCACCGTGCCTGACCTGCTGCTGGCGCTGGTGTCTCTGGAGCTGTGGTG 315
QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
Db 316 GGAATATACCCCTCAGGGGTATTGGAGCTGTGCTCCCTCACCTAGGGACAGGGAGAGA 375
QY 41 AspSerValCysProGlnCysLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
Db 376 GATAGTGTGTGCCCAAGGAATAATATCCACCTCAAAATAATTCGATTTCGTGTACC 435
QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlnAspThrAsp 80
Db 436 AAGTCCACAAAGGAACCTACTTGTACATGACTGTCTCCAGGCGGGCAGGATACGGAC 495
```


QY	21	GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg	40
DB	316	GGAAATATACCCCTCAGGGGGTTATTGGACATGGTCCCTCACCTAGGGACAGGGAGAGAGA	375
QY	41	AspSerValCysProGlnGlyLysTyrIleHisProGlnAnsnAnSerIleCysCysThr	60
DB	376	GATAGTGTGTGTCGCCAAGGAAATATATCCACCCTCAAAATAATTCGATTGTGTGTTACC	435
QY	61	LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp	80
DB	436	AAGTGCCCAAAAGGAACTACTTGTACATYAGACTGTCCAGGCCCGGGCAGGATACGGAC	495
QY	81	CysArgGluCysGluSerGlySerPheThrAlaSerGluAnsnHisLeuArgHisCysLeu	100
DB	496	TGCAGGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACTCAGACACTGCCTC	555
QY	101	SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp	120
DB	556	AGCTGCTCCAAATGCCAAAGGAAATGGGTCAAGTGGAGATCTCTTCTTGACACAGTGGAC	615
QY	121	ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTTPSerGluAnsnLeu	140
DB	616	CGGGACACCGTGTGGCTGCAGAGAAACCACTGACCGGCATTTATTTGGAGTGAANAACCTT	675
QY	141	PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu	160
DB	676	TTCCAGTGTCTCAATTGTCAGGCTCTGCCTCAATGGGACCGTGCACCTCTCTCTGCCAGGAG	735
QY	161	LysGlnAnsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAnsnGluCysVal	180
DB	736	AAACAGAAACACCGTGTCCACCTGCCATGCAGGTTTCTTTAAGAGAAAAACGAGTGTGTC	795
QY	181	SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu	200
DB	796	TCCTGTAGTAACCTAGAAAAGCCTGGAGTGCACGAAGTTGTGCCCTACCCCAAGATTGAG	855
QY	201	AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe	220
DB	856	AATGTTAAGGCACTGAGGACTCAGGCACCACTAGTGTGTTGGCCCTGGTCAATTTCTTT	915
QY	221	GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrrLys	240
DB	916	GGTCTTTGGCCCTTTATCCCTCCCTCTTCATTTGGTTTAAATGTATCGCTACCAACGGTGAAG	975
QY	241	SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu	260
DB	976	TCCAAGCTCTACTCCATTTGTTGGGAATCGACACTGAAAAGAGGGGAGCTTGAA	1035
QY	261	GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr	280
DB	1036	GGAACTACTACTAAGCCCTTGGGCCCAAAACCCAAAGCTTCAGTCCCACTCCACCTATACC	1095
QY	281	ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr	300
DB	1096	CCACCCCTGGGCTTCAGTCCCGTGCCAGTTCCACCTTCACCTCCACCTCCACCTATACC	1155
QY	301	ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly	320
DB	1156	CCCGGTGACTGTCCCACTTTGGGGTCCCGCCAGAGAGGTGGCACCACTATACAGGGG	1215
QY	321	AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys	340
DB	1216	GCTGACCCCATCTTGGACAGCCCTCGCCTCCGACCCCATCCCAACCCCTTCAGAAG	1275
QY	341	TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr	360
DB	1276	TGGGAGACAGCCGCCAACAGCACAGAGCTTAGACACTGATGACCCCGCGAGCGCTGTAC	1335
QY	361	AlaValValGluAnsnValProProLeuArgTrrLysGluPheValArgArgLeuGlyLeu	380
DB	1336	GCCGTGTGTGAAGAACGTGCCCGCTGGAGGAAGAAATTCGTGGCGGCCCTAGGGCTG	1395
QY	381	SerAspHisGluIleAspArgLeuGluLeuGlnAnsnGlyArgCysLeuArgGluAlaGln	400

Db	1396	AGCGACCAAGAGATCGATCGCTGGAGCTGCAGAACGGGGCGCTGCCTGCGGAGGCGCAA	1455
Qy	401	TyrSerMetLeuAlaThrThrAspArgArgThrProArgArgGluAlaThrLeuGluLeu	420
Db	1456	TACAGCATGCTGGCGACCTGGAGGCGCGCACGCCGCGCGGAGGCCACGCTGGAGCTG	1515
Qy	421	LeuGlyArgValLeuArgMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla	440
Db	1516	CTGGAGCGCTGCTCCGCGACATGGAGCTGCTGGCTGCTCGAGACATCGAGGAGGCG	1575
Qy	441	LeuCysGlyProAlaLeuLeuProProAlaProSerLeuLeuArg	455
Db	1576	CTTTGGCGCGCGCGCGCTCCGCGCGCGCCAGTCTTCTCAGA	1620
RESULT	10		
LOCUS	A43873	2175 bp	DNA linear PAT 06-MAR-1997
DEFINITION	Sequence 1 from Patent EP0657536.		
ACCESSION	A43873		
VERSION	A43873.1	GI:2299022	
KEYWORDS	unidentified.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 2175)		
AUTHORS	Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.		
TITLE	Proteases capable of shedding the soluble TNF-receptor and TNF-R derived peptides and antibodies against the proteases inhibiting the shedding		
JOURNAL	Patent: EP 0657536-A 1 14-JUN-1995;		
COMMENT	YEDA RES & DEV (IL) Other publication ZA 9407962 951121 Other publication JP 7194376 950801 Other publication AU 7574294 950504 Other publication CA 2133872 950413.		
FEATURES	Location/Qualifiers		
source	1..2175		
CDS	/organism="unidentified" /db_xref="taxon:32844" 256..1623 /note="unnamed protein product" /codon_start=1 /protein_id="CAA02771.1" /db_xref="GI:2299023" /translation="MGLSVFVPLLPLVLELLVGYPSGVILGPHZGDRKRSVCPQKYLHPQNNISICCTKCHGTYLYNDPCPGQDTCRECSGFTASENHLRHCLSCSKRCKEMGQVEISCTVDRDTCGCKNKQRYHWSENLPQCFNCSLNGTVHLSCQEKONTCTHAGFTFLRENECVSCNCKNLEKTLCLPQIENVKGTEDSGTTLPLVIFPGICLLSLFLGLMTRYORWKSPLYSVCGKSTPEKEGELGTTTKPLAPNPSPFTPGPTLGLSPSSFTSSSTVTPGDCNFAAPREVAAPPYGGADPILATALASDPIPNLQKWDASAHPQSLDDDDPATLYAVVENVPPLRWKEFVRGLSHDEIDRLRLQNGRCREAGTSMLATWARRTPRRATLELLGRVLRMDLLGCLIEDIEELALCGPALUPPA		
BASE COUNT	474 a 641 c 604 g 456 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	2,99e-154	Length:	2175
Score:	2487.00	Matches:	455
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-09-899-422A-2 (1-455) x A43873 (1-2175)			
Qy	1	MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuLeuVal	20
Db	256	ATGGGCTCTCCACCGGCGCTGACCTGCTGCCCTGGTCTCTCGAGCTGTGGTG	315
Qy	21	GlyTleYrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluYsArg	40

QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 676 TTCAGTGTCTCAATTCAGAGCTCTGCCTCAATGGAGCGTGACCTCTCTCCGCCAGGAG 735
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db 736 AACAGAACACCGTGTGCACCTGCCATGCAGGTTCTTTCTAAGAGAAACAGAGTGTGC 795
QY 181 SerCysSerAsnCysGlyLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 796 TCCTGTAGTAACTGAAGAAAGCCTGGAGTGCAGGAAGTTGTGCTACCCAGATTGAG 855
QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuProLeuValIlePhePhe 220
Db 856 AATGTTAAGGGCACTGAGAGCTCAGGCACACAGTGTGTGCTGCTGCTATTTCTTT 915
QY 221 GlyLeuCysLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
Db 916 GGTCTTTGCCITTTATCCCTCTCTCATTTGTTAATGTATCGTACCAACGGTGGAG 975
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGluLeuGlu 260
Db 976 TCCAAGCTCTACTCCATTGTTGTGGAAATCGACACCTGAAAAAGAGGGGAGCTTGA 1035
QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 1036 GGAATCTACTTACCCCTTGCCCTCCCAACCCAGCTTCAGTCCACCTCCAGCTTAC 1095
QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300
Db 1096 CCCACCTTGGGCTTCAGTCCCGTCCAGTTCACCTTCACCTCCAGCTCCACCTATACC 1155
QY 301 ProGlyAspCysProAsnPheAlaProArgArgGluValAlaProProTyrGlnGly 320
Db 1156 CCCGTGTACTTCCCACTTTCGGCTCCCGCAGAGAGTGGCACCCCTATCAGGGG 1215
QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
Db 1216 GCTGACCCCATCTTGGCAGAGCCCTCGCTCCGACCCCTCCACCCCTTCGAGAG 1275
QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
Db 1276 TGGAGGACAGCGCCCAAGCCACAGAGCTAGACACTGATGACCCCGCAGCGTATC 1335
QY 361 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu 380
Db 1336 GCCGTGGTGGAGAGCTGCCCTGCTGGCTGGAGGAATTCGTGCGCGCTAGGGCTG 1395
QY 381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
Db 1396 AGCGACACAGATCGATCGCTGGAGTGCAGAACGGCGCTGCTGCGCGAGCGGCA 1455
QY 401 TyrSerMetLeuAlaThrTrpArgArgThrProArgArgGluAlaThrLeuGluLeu 420
Db 1456 TACAGCATGCTGGCGACCTGGAGGGCGGCACCGCGCGCGAGGCCACCGTGGAGCTG 1515
QY 421 LeuGlyArgValLeuArgAspMetAspLeuGlyCysLeuGluAspIleGluAla 440
Db 1516 CTGGAGCGCTGCTCCCGACATGACCTGCTGGGCTGCTGGAGGACATCGAGGAGCG 1575
QY 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
Db 1576 CTTTGGGCGCGCGCGCTCCCGCGCGCGCTCTCTCAGA 1620

RESULT 12
AR041076
LOCUS AR041076 2175 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5811261.
ACCESSION AR041076
VERSION AR041076.1 GI:5961572
KEYWORDS Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 2175)
AUTHORS Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and Aderka,D.
TITLE Expression of the recombinant tumor necrosis factor binding protein I (TBP-I)
JOURNAL Patent: US 5811261-A 1 22-SEP-1998;
FEATURES Location/Qualifiers
source 1..2175
BASE COUNT 474 a 641 c 604 g 456 t
ORIGIN
Alignment Scores:
Score: 2,99e-154 Length: 2175
Pred. No.: 2487.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-899-422A-2 (1-455) x AR041076 (1-2175)
QY 1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuLeuVal 20
Db 256 ATGGGCCCTCTCCACCGTGCCTGACCTGCTGCTGCGGCTGGTCTCCTCGAGCTGTGGTG 315
QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
Db 316 GGAATATACCTCCTCAGGGGTATTGGACTGGTCCCTCCTACCTAGGGACAGGAGAGAGA 375
QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
Db 376 CATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTTCGTGTACC 435
QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
Db 436 AAGTCCCAAGAGGAACTACTTGTACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 495
QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db 496 TGCAGGAGTGTGAGAGCGGCTCTTCCACCGCTTCAGAAACACCTCAGACACTGCCTC 555
QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db 556 AGCTGCTCAATCCGAAAGGAAATGGGTGAGTGGAGATCTCTTCTGCACAGTGGAC 615
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
Db 616 CGGACACCGTGTGGCTGCAGGAAGAACAGTACCGGCAATATTGGAGTGAACACCTT 675
QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 676 TTCCAGTGTCTCAATTCAGAGCTCTGCCTCAATGGACCGTGCACCTCTCCTGCCAGAG 735
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db 736 AACAGAACACCGTGTGCACCTGCCATGCAGGTTCTTTCTAAGAGAAACAGAGTGTGC 795
QY 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 796 TCCTGTAGTAACTGAAGAAAGCCTGGAGTGCAGGAAGTTGTGCTACCCAGATTGAG 855
QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
Db 856 AATGTTAAGGGCACTGAGGACTCAGGCACACAGTGTGTGCTGCTGCTGCTGCTGCTTCTTT 915
QY 221 GlyLeuCysLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
Db 916 GGTCTTTGCCITTTATCCCTCTCTCATTTGTTAATGTATCGTACCAACGGTGGAG 975
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGluLeuGlu 260

976	TCCAAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGAA	1035
261	GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr	280
1036	GGAACCTACTACTAAGCCCTCGCCCAACCAAGCTTCAGTCCACTCCAGGCTTCACC	1095
281	ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrTyrThr	300
1096	CCACCTCTGGGCTTCAGTCCGCTGCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC	1155
301	ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly	320
1156	CCGGTGACTGTCACCACTTTGGGGTCCCGCAGAGAGTGCACCACTATCAGGGG	1215
321	AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys	340
1216	GCTGACCCCATCTTGGGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAAG	1275
341	TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr	360
1276	TGGGAGGACAGCGCCACAAAGCCACAGAGCTTAGACACTGATGACCCCGGAGCGTGAC	1335
361	AlaValValGluAsnValProProLeuArgTyrLysGluPheValArgLeuGlyLeu	380
1336	GCGTGTGGAGNACGTGCCCCGTTCGCTGGAGAGATTCGTGGGGCCCTAGGCGTG	1395
381	SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln	400
1396	AGCGACACGAGATCGATCGCTGGAGCTGCAGAACGGCGCTGCTGCGAGCGCAA	1455
401	TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu	420
1456	TACAGCATGCTGGCGACCTGGAGCGCGCCACCGCGCGGCGAGCCACGCTGGAGCTG	1515
421	LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla	440
1516	CTGGACGGCTGCTCCGCGACATGGACCTGCTGGGGTGGCTGGAGGACATCGAGGAGCG	1575
441	LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg	455
1576	CTTTGGGGCCCGCCCTCCCGCCCGCCCGCCAGTCTTCTCAGA	1620
RESULT 13		
164751		
LOCUS	164751	2175 bp DNA linear PAT 07-OCT-1997
DEFINITION	Sequence 1 from patent US 5665859.	
ACCESSION	164751	
VERSION	164751.1 GI:2481645	
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 2175)	
AUTHORS	Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.	
TITLE	Molecules influencing the shedding of the TNF receptor, their preparation and their use	
JOURNAL	Patent: US 5665859-A 1 09-SEP-1997;	
FEATURES	Location/Qualifiers	
source	1..2175	
	/organism="unknown"	
BASE COUNT	474 a	641 c 604 g 456 t
ORIGIN		
Alignment Scores:		
Pred. No.:	2.99e-154	Length: 2175
Score:	2487.00	Matches: 455
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	6	Gaps: 0
US-09-899-422A-2 (1-455) x 164751 (1-2175)		

```
Db 1336 GCGGTGGTGGAGACGTGCCCCGTGGCGTGGAGGAATTCGTGGCGGCTAGGGCTG 1395
QY 381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
Db 1396 ACCGACACAGATCGATCGGTGGAGTGCAGACAGGGCGTGGCTGGCGGAGGCGCA 1455
QY 401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
Db 1456 TACAGCATGCTGGCGACCTGGAGGCGGCACACCGCGCGGCGAGGCCACGCTGGAGCTG 1515
QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
Db 1516 CTGGGACGGTGTCCGGACATGAGCTGTGGGTGGCTGGAGGACATCGAGGAGCG 1575
QY 441 LeuGlyGlyProAlaAlaLeuProAlaProSerLeuLeuArg 455
Db 1576 CTTTGGGCGCGCGCGCTCCGCGCGGCGCCAGCTCTTCAGAGA 1620

RESULT 14
LOCUS A19907 2176 bp DNA linear PAT 04-OCT-1994
DEFINITION Synthetic nucleotide sequence Type I TNF receptor gene.
ACCESSION A19907
VERSION A19907.1 GI:641222
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 2176)
AUTHORS Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and Aderka,D.
TITLE Expression of the recombinant tumor necrosis factor binding protein I (TBP-I)
JOURNAL Patent: EP 0433900-A 28 JUN-1991;
FEATURES source
location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 474 a 642 c 604 g 456 t
ORIGIN

Alignment Scores:
Pred. No.: 2,99e-154 Length: 2176
Score: 2487.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-899-422A-2 (1-455) x A19907 (1-2176)
QY 1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuLeuVal 20
Db 256 ATGGCCCTCTCCACGTCGCTGACCTGCTGCTGGCGCTGGTGGTGGTGGTGGT 315
QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGlyLysArg 40
Db 316 GGAATATACCCCTCAGGGGTATTGGACTGTGCTCCCTACCTAGGGGACAGGAGAGA 375
QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
Db 376 GATAGTGTGTGCCCAAGSAAATATATCCACCTCAAAAATAATTGCTGTGTACC 435
QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
Db 436 AAGTGCACCAAGGACCTACTTGTACAACTGCTCCAGGCCCGGGGACGATACGGAC 495
QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db 496 TGCAGGAGTGTGAGAGGGGCTCCTTCACCGCTTCAGAAAAACCACTCAGACACTGCCTC 555
```

```
QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db 556 AGCTGCTCCAAATCCGAAAGGAAATGGGTAGGTGGAGATCTCTTCTTCACAGCTGGAC 615
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
Db 616 CGGGACACCGTGTGGGTGTCAGAGAACACCACTACCGGCATTAATTGGAGTGAAACCTT 675
QY 141 PheGlnCysPheAsnCysSerLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 676 TTCAGTGTCTCAANTGACGCTCTGCTCAATGGACCGTGCACCTCTCTCTGCCAGGAG 735
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db 736 AAACAGAACACCGTGTGACCTGCCATGCAGGTTCTTTCTTAAGAGAAACAGAGTGTGTC 795
QY 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 796 TCCTGTAGTAACGTGAAGAAAGCCGTGGAGTGCACAAAGTTGTGCTTACCCAGATTGAG 855
QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
Db 856 AATGTTAAGGACACTGAGGACTCAGCACACACAGTGTGTCCTCCCTGCTCATTTCTTT 915
QY 221 GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
Db 916 GGTCTTTGCTTTTATCCTCTCTCTTCTTATGTTTAAATGATCGTACCAACGGTGAAG 975
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeuGlu 260
Db 976 TCCAAAGCTCTACTCCATTTGTTGTGGAAATCGACACCTGAAAGAGGGGAGGTTGAA 1035
QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 1036 GGAATACTACTAAGCCCTTGGCCCAACCAAGCTTCAGTCCCACTCCAGCTTCAC 1095
QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrThr 300
Db 1096 CCCACCTGGGCTTCAGTCCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1155
QY 301 ProGlyAspCysProAsnPheAlaAlaProArgGluValAlaProProTyrGlnGly 320
Db 1156 CCCGTGACTGTCCCACTTTGCGGCTCCCGCAGAGAGTGGCACCACTATACAGGGG 1215
QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
Db 1216 GCTGACCCCATCTTGGCGACAGCTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1275
QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspProAlaThrLeuTyr 360
Db 1276 TGGGAGGACAGCGCCACAGCCACAGAGCTAGACACTGATGACCCGCGACGCTGTAC 1335
QY 361 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgLeuGlyLeu 380
Db 1336 GCGGTGTGTGAGAACGTGCCCTTGGCTGGAGGAATTCGTGGCGGCTAGGGCTG 1395
QY 381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
Db 1396 AGCGACACAGAGATCGATCGCTGGAGTGCAGAACGGCGCTGCTGCGGAGGCGCA 1455
QY 401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
Db 1456 TACAGCATGCTGGGACCTGGAGGCGGCACCGCGCGGCGGAGGCGGAGCTG 1515
QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
Db 1516 CTGGGACGGTGTCCGGACATGAGCTGTGGGTGGCTGGAGGACATCGAGGAGCG 1575
QY 441 LeuCysGlyProAlaAlaLeuProAlaProSerLeuLeuArg 455
Db 1576 CTTTGGGCGCGCGCGCTCCGCGCGGCGCCAGCTCTTCAGAGA 1620

RESULT 15
```

BC010140
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BC010140
Homo sapiens, tumor necrosis factor receptor superfamily, member 1A, clone MGC:19588 IMAGE:4131360, mRNA, complete cds.
BC010140
BC010140.1 GI:14603367
MGC.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2194)
Strausberg,R.
Direct Submission
Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R., Lim,M., Maduro,Q.L., Mastello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J., Tjongson,E.E., Touchman,J.W., Tsurgueon,C., Vogt,J.L., Walker,M.A., Zhang,L.-H. and Green,E.D.

REMARK
COMMENT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 27 Row: m Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 339755.
FEATURES
source
Location/Qualifiers
1..2194
/organism="Homo sapiens"
/db_xref="LocusID:7132"
/db_xref="taxon:9606"
/clone="MGC:19588 IMAGE:4131360"
/tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
241..1608
/codon_start=1
/product="tumor necrosis factor receptor superfamily, member 1A"
/protein_id="AAH0140.1"
/db_xref="GI:14603368"
/translation="MGLSTVPLDLLLVLELLVGVPSGVLVPHVLDREKRDVSC
POKYLHPQNNSTCCCKHKGTYLYNDKCPGQDTCRCESGSFTASENHLRCLSC
SKRKEQGVSEISCVDRYTCGRKNQYRHWSENLCFCNCLNGTVHLSCQE
KQVTCCHAGFLRENEVCSCNKRSLCTKLCUPQIENVRGTEGSDGTVLLPLVI
FFGLCLLGLFGLMYRQWKSLEYVCGKSTPEKEGELEGTTKPLAPNFSFPT
PNPGLTGFSPVSSSTSTPGCPNFAAPRREVPYQCAPLATALASDPI
PNPLQWESAHKPSQSLDTPATLVAVENVPRLRWKEFVRLGLSDHIDLELQN
GRCLREAYSMLATWRRRTPRRENTLELLGRVLRDMDLLGLEIEALCGPALPPA
PSLLR"

CDS
BASE COUNT
ORIGIN
Alignment Scores:
Pred. No.:
Score:

478 a 644 c 600 g 472 t
3.02e-154 Length: 2194
2487.00 Matches: 455

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9	Indels:	0
DB:	9	Gaps:	0
US-09-899-422A-2 (1-455) x BC010140 (1-2194)			
QY	1	MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuLeuVal	20
Db	241	ATGGGGCTCTCCACCGCTGCTGACCTGCTGCCACTGCTGCTGGAGCTGTGGTG	300
QY	21	GlyLeuProSerGlyValLeuGlyLeuValProHisLeuGlyAspArgGlyLeuArg	40
Db	301	GGAAATATACCCCTCAGGGGTATTGGACTGGTCCCTCACCTAGGGGACAGGAGAGA	360
QY	41	AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysThr	60
Db	361	GATAGTGTGTGTCGCCAGGAAATATATCCACCTCAANAATATTCGATTTGCTGACC	420
QY	61	LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThr	80
Db	421	AAGTGCACAAAGGAACCTACTTGTACAATGACTGTCCAGCGCCGGGACGATACGAC	480
QY	81	CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu	100
Db	481	TGCAGGAGTGTGAGAGCGGCTCTTCAACCGCTTCAGAAACACCTCCAGACACTGCCTC	540
QY	101	SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValasp	120
Db	541	AGCTGCTCAAAATGCCGAAGAAATGGGTGAGTGGAGATCTCTTTCACACAGTGGAC	600
QY	121	ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu	140
Db	601	CGGGACACCGCTGTGCTGCAGGAGAACAGTACCGCATATTATGGAGTGAACACCTT	660
QY	141	PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu	160
Db	661	TTCCAGTGTCTCAATTGCAGCGCTCTGCCTCAATGGGACCGTGCCTTCTGCGACGAG	720
QY	161	LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysVal	180
Db	721	AAACAGAACCGGTGTCACCTGCCATGCAGGTTCTTCTTAAGAGAAACAGAGTGTGTC	780
QY	181	SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu	200
Db	781	TCCTGTAGTAACCTAGAGAAAGCCTGGAGTGCAGCAAGTTGTGCTTACCCACGATGAG	840
QY	201	AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe	220
Db	841	AATGTTAAGGGCACTGAGGACTCAGGCACACAGTGTGTGCCCCCTGGTCAATTTCTTT	900
QY	221	GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTyrLys	240
Db	901	GGTCTTTGCTTTTATCCCTCTCTTCAATGGTTAATGATGCTACCAACAGGTGGAG	960
QY	241	SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeuGlu	260
Db	961	TCCAAGCTCTACTCCATTGTTGTGGAAATCGACACTGAAAGAGGGGAGCTTGAA	1020
QY	261	GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr	280
Db	1021	GGAACTACTACTAAGCCCTTGGCCCCCAACCAAGTTCAGTCCCACTCCAGGCTTCACC	1080
QY	281	ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrTyrThr	300
Db	1081	CCACCTTGGGCTTCACTCCGCGCCAGTTCCACCTTCCACTCCAGCTCCACCTATACC	1140
QY	301	ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly	320
Db	1141	CCGGTCACTGTCCCAACTTTGCGCTCCCGCAGAGAGGTGGCACCACCTATCAGGG	1200
QY	321	AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys	340

1201	Db	CTGTGACCCCATCTTGGCAGACAGCCCTCGCTCGCATCCCAACCCCATCCCAACCCCTTCAGAAG	1260
341	Qy	TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr	360
1261	Db	TGGAGGACAGCGCCACACAGCCACAGAGCTAGACACTGATGACCCCGCGAGCGCTGTAC	1320
361	Qy	AlaValValGluAsnValProProLeuArgTTPlysGluPheValArgArgLeuGlyLeu	380
1321	Db	GCCTGTGTGGAGAACGTGCCCGCTTGCCTGGAAGGAATCTGCTGGCGGCGCTAGGCGCTG	1380
381	Qy	SerAspHisGlnIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln	400
1381	Db	AGCGACACAGAGATCGATCGCTGGAGCTGCAGAACGGCGCTGCCTGGCGAGGCGCAA	1440
401	Qy	TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu	420
1441	Db	TACAGCATGCTGGGACCTGGAGCGCGGCGACGCCCGGCGCGAGGCCACGCTGGAGCTG	1500
421	Qy	LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla	440
1501	Db	CTGGAGCGCTGTCTCCGCACATGGACCTGCTGGGCTGCCTGGAGGACATCGAGGAGCG	1560
441	Qy	LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg	455
1561	Db	CTTTGGGGCCCCGCCCTTCGGCGCGCGCGCCAGCTCTCTCAGA	1605

Search completed: June 9, 2003, 02:13:37
Job time : 3023 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 20:48:38 ; Search time 1864 seconds
(without alignments)
11885.958 Million cell updates/sec

Title: US-09-899-422A-1
Perfect score: 1368
Sequence: 1 atggcctctccacgtgcc.....cgccagttcttcagatga 1368

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hctc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hctc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	809.8	59.2	1076	14	BM923204
2	803.6	58.7	931	14	BQ723672
3	764.6	55.9	957	9	AL559050
4	703.6	51.4	741	13	BI860918
5	689	50.4	889	9	AU117362
6	682.4	49.9	761	9	AU131978

7	680	49.7	942	9	AL529836
8	679.8	49.7	1070	13	BM546826
9	678.2	49.6	975	9	AL577008
10	669	48.9	669	14	BM742388
11	668.6	48.9	974	12	BG180101
12	667.8	48.8	696	14	BM989994
13	667	48.8	718	12	BG680679
14	647.2	47.3	994	14	BM800044
15	638.4	46.7	837	9	AL522989
16	630.4	46.1	769	9	AL522226
17	628.6	46.0	916	13	BI757305
18	625	45.7	636	12	BG035257
19	620.4	45.4	1131	13	BM467058
20	605.4	44.3	818	13	BI821169
21	605.2	44.2	969	12	BE871809
22	602	44.0	602	14	BM791206
23	601.4	44.0	643	12	BG680356
24	596.2	43.6	859	13	BI870917
25	590.8	43.2	627	14	BM763879
26	588	43.0	811	12	BF342334
27	585.4	42.8	872	13	BI769006
28	576	42.1	576	14	BM820201
29	573.4	41.9	575	14	BM705174
30	564	41.2	845	9	AU125021
31	559.4	40.9	739	13	BI520191
32	559	40.9	859	9	AU124446
33	559	40.9	936	12	BG681438
34	557.2	40.7	872	14	BQ723589
35	556.6	40.7	767	9	AU142156
36	549	40.1	549	14	BM708362
37	546	39.9	546	14	BM782977
38	542	39.6	1055	13	BM555065
39	541.8	39.6	915	14	BQ881180
40	541.4	39.6	702	12	BF344496
41	541	39.5	971	12	BE876920
42	540.6	39.5	772	9	AU137990
43	533.6	39.0	823	13	BI766980
44	530.4	38.8	532	14	BM755879
45	529.4	38.7	1008	14	BQ719773

ALIGNMENTS

RESULT 1
BM923204
LOCUS BM923204 1076 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6625801 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5758757
5', mRNA sequence.
ACCESSION BM923204
VERSION BM923204.1 GI:19373583
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1076)
NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

JOURNAL

Contact: Robert Strausberg, Ph.D.
Email: cygabs-remail.nih.gov

COMMENT

Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL2803 row: b column: 06
High quality sequence stop: 727.
Location/Qualifiers
I. .1076

FEATURES

source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5758757"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
/notes="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH MGC Library."
BASE COUNT      206 a   356 c   303 g   205 t     6 others
ORIGIN
Query Match
Best Local Similarity 59.2%; Score 809.8; DB 14; Length 1076;
Matches 811; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 553 TGTAGAAAGCCTGGAGTGCACGAAGTTGGCTTACCCAGATTGAGAATGTTAAGGC 612
DB 14 TGTAGAAAGCCTGGAGTGCACGAAGTTGGCTTACCCAGATTGAGAATGTTAAGGC 73
QY 613 ACTGAGGACTCAGGCACACAGTGTGTGGCCCTGGTTCATTTCTTGGTCTTTGCCCT 672
DB 74 ACTGAGGACTCAGGCACACAGTGTGTGGCCCTGGTTCATTTCTTGGTCTTTGCCCT 133
QY 673 TTATCCCTCCTCTTCATTTGGTTTAAATGATCGTACCAACGGTGGAGTCCCAAGCTTAC 732
DB 134 TTATCCCTCCTCTTCATTTGGTTTAAATGATCGTACCAACGGTGGAGTCCCAAGCTTAC 193
QY 733 TCCATTGTTTGGGAATGCACACCTGAAAAGAGGGGGAGCTTGAAGAACTACTACT 792
DB 194 TCCATTGTTTGGGAATGCACACCTGAAAAGAGGGGGAGCTTGAAGAACTACTACT 253
QY 793 AAGCCCTTGGCCCAAAACCCAGCTTCAGTCCACTCCAGCTTCACCCACCCACCCCTGGGC 852
DB 254 AAGCCCTTGGCCCAAAACCCAGCTTCAGTCCACTCCAGCTTCACCCACCCACCCCTGGGC 313
QY 853 TTCAGTCCCGTCCGAGTTCACCTTCACCTTCAGTCCAGTCCACTATACCCCGGGTACTGT 912
DB 314 TTCAGTCCCGTCCGAGTTCACCTTCACCTTCAGTCCAGTCCACTATACCCCGGGTACTGT 373
QY 913 CCCAACTTTGGGCTCCCGCAGAGAGTGGCCACACCCCTATCAGGGGGCTGACCCCATC 972
DB 374 CCCAACTTTGGGCTCCCGCAGAGAGTGGCCACACCCCTATCAGGGGGCTGACCCCATC 433
QY 973 CTTGGCAGAGCCTCGCCTCCGACCCCATCCCAACCCCTTCAGAGTGGGAGACAGC 1032
DB 434 CTTGGCAGAGCCTCGCCTCCGACCCCATCCCAACCCCTTCAGAGTGGGAGACAGC 493
QY 1033 GCCCAAGCCACAGAGCCTAGACACTGATGATGACCCCGCAGCCTGTACGCCGTGGTGGAG 1092
DB 494 GCCCAAGCCACAGAGCCTAGACACTGATGATGACCCCGCAGCCTGTACGCCGTGGTGGAG 553
QY 1093 AACGTGCCCGTTCGCTGGAAGAAATTCGTGGCGGCCCTAGGCTGAGCCACACAG 1152
DB 554 AACGTGCCCGTTCGCTGGAAGAAATTCGTGGCGGCCCTAGGCTGAGCCACACAG 613
QY 1153 ATCGATCGGCTGGAGCTGCAGAAAGGGGCTGCCTTCGCGAGGGCGCAATACAGATGCTG 1212
DB 614 ATCGATCGGCTGGAGCTGCAGAAAGGGGCTGCCTTCGCGAGGGCGCAATACAGATGCTG 673
QY 1213 CGGACCTGGAGGGCGGCACCGCGCGGCGAGCCAGCGTGGAGCTGCTGGGAGCGCTG 1272
DB 674 CGGACCTGGAGGGCGGCACCGCGCGGCGAGCCAGCGTGGAGCTGCTGGGAGCGCTG 733
QY 1273 CTCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGAGGCGCTTGGGGCCCC 1332

```

```

DB 734 CTCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGANGCCTTTGNGCCCC 793
QY 1333 GCCGCCCTCCCGCCGCCGCCAGTCTTCTCAGATGA 1368
DB 794 GNGGCCCTCCCGCCGCCGCCAGTCTTCTCAGATGA 829

RESULT 2
LOCUS      B0723672          931 bp      mRNA      linear      EST 16-JUL-2002
DEFINITION AGENCOURT_849850 Lupski_dorsal_root_ganglion Homo sapiens CDNA
ACCESSION  B0723672
VERSION    B0723672
KEYWORDS   B0723672.1 GI:21862569
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 931)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Dr. James R. Lupski
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13573 row: d column: 24
            High quality sequence stop: 607.

FEATURES             Location/Qualifiers
     source            1..931
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6184295"
                     /clone_lib="Lupski_dorsal_root_ganglion"
                     /sex="male"
                     /tissue_type="dorsal root ganglia"
                     /dev_stage="adult, 36 yr"
                     /lab_host="DH10B"
     note              Note: Vector: pCMV-SPORT6 (Life Technologies); Site_1:
                     NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                     Directionally cloned using the following adaptors:
                     5'-TCGACCCACGCGTCCG-3' and
                     5'-GACTAGTTCAGATCGCGAGCGGCGCT(15)-3'. Size selected >
                     1 kb for average insert length 1.7 kb. This is a primary
                     library, non-amplified. Library constructed by Life
                     Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                     College of Medicine) and is available through Life
                     Technologies.
BASE COUNT      218 a   283 c   224 g   204 t     2 others
ORIGIN
Query Match
Best Local Similarity 58.7%; Score 803.6; DB 14; Length 931;
Matches 862; Conservative 0; Mismatches 40; Indels 5; Gaps 3;
QY 111 GGAGAAGAGATAGTGTGTCTCCCAAGGAAATATATCCACCTCAAAATATTCAT 170
DB 1 GGAGAAGAGATAGTGTGTCTCCCAAGGAAATATATCCACCTCAAAATATTCAT 60
QY 171 TTGCTGTACCAAGTGCACAAAGAACCTACTTGTACATGACTGTCCAGCCCGGGGCA 230
DB 61 TTGCTGTACCAAGTGCACAAAGAACCTACTTGTACATGACTGTCCAGCCCGGGGCA 120
QY 231 GGATACGACTGCGGGAGTGTGAGCGGCTCTTCCCGCTTCAGAAAACACCTCAG 290
DB 121 GGATACGACTGCGGGAGTGTGAGCGGCTCTTCCCGCTTCAGAAAACACCTCAG 180

```


FEATURES	Location/Qualifiers
source	1..957
291	ACACTGCTCAGCTGCTCAATATGCGGAAAGAAATGGTGCAGTGGAGATCTCTTTG 350
181	ACACTGCTCAGCTGCTCAATATGCGGAAAGAAATGGTGCAGTGGAGATCTCTTTG 240
351	CACAGTGGACGGGACACGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 410
241	CACAGTGGACGGGACACGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
411	TGAACACCTTTTCCAGTGTCTCAATATGCGGAAAGAAATGGTGCAGTGGAGATCTCTTTG 470
301	TGAACACCTTTTCCAGTGTCTCAATATGCGGAAAGAAATGGTGCAGTGGAGATCTCTTTG 360
471	CTGCCAGGAGAAACAGACACGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 530
361	CTGCCAGGAGAAACAGACACGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
531	CGAGTGTCTCTCTGAGTGTCTCAATATGCGGAAAGAAATGGTGCAGTGGAGATCTCTTTG 590
421	CGAGTGTCTCTCTGAGTGTCTCAATATGCGGAAAGAAATGGTGCAGTGGAGATCTCTTTG 480
591	CCAGATTGAGATGTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 650
481	CCAGATTGAGATGTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
651	CATTTCCTTTGCTCTCTGAGTGTCTCAATATGCGGAAAGAAATGGTGCAGTGGAGATCTCTTTG 710
541	CATTTCCTTTGCTCTCTGAGTGTCTCAATATGCGGAAAGAAATGGTGCAGTGGAGATCTCTTTG 600
711	ACGGTGGAGTCCAGCTCTACTGAGTGTCTCAATATGCGGAAAGAAATGGTGCAGTGGAGATCTCTTTG 770
601	ACGGTGGAGTCCAGCTCTACTGAGTGTCTCAATATGCGGAAAGAAATGGTGCAGTGGAGATCTCTTTG 660
771	GGAGCTTGAAGGAGTCTACTGAGTGTCTCAATATGCGGAAAGAAATGGTGCAGTGGAGATCTCTTTG 830
661	GGAGCTTGAAGGAGTCTACTGAGTGTCTCAATATGCGGAAAGAAATGGTGCAGTGGAGATCTCTTTG 720
831	AGGCTTACCCACCCAGCTG-GGCTTACGTCGCGGAGGAGGAGGAGGAGGAGGAG 889
721	AGGCTTACCCACCCAGCTG-GGCTTACGTCGCGGAGGAGGAGGAGGAGGAGGAG 780
890	CCACCTATA-CCCGCGGAGTCTCCAGCTTGGG-CTCCCGCGGAGGAGGAGGAGGAG 945
781	CCACCTATA-CCCGCGGAGTCTCCAGCTTGGG-CTCCCGCGGAGGAGGAGGAGGAG 840
946	CCACCTATA-CCCGCGGAGTCTCCAGCTTGGG-CTCCCGCGGAGGAGGAGGAGGAG 1005
841	CACCCCTATCAGGGGGCTGACCCCATCTTGGAGAGGAGGAGGAGGAGGAGGAG 900
1006	AACCCCT 1012
901	CATTCCC 907
RESULT 3	
LOCUS	AL559050
DEFINITION	AL559050 LTI_NFL008_Tc2 Homo sapiens cDNA clone CS0D0J010YB05 5 prime, mRNA sequence.
ACCESSION	AL559050
VERSION	AL559050.1 GI:12904166
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1. (bases 1 to 957)
TITLE	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
JOURNAL	Full-length cDNA libraries and normalization
COMMENT	Unpublished (2001)
	Contact: Genoscope
	Genoscope - Centre National de Sequencage
	BP 191 91006 EVRY cedex - France
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.


```
Query Match 50.4%; Score 689; DB 9; Length 889;
Best Local Similarity 99.4%; Pred. No. 1.5e-159;
Matches 700; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 665 TTGCGCTTTATCCCTCCCTCTCATTTGTTTAAATGATCGCTACCAACGGTGGAGTCCA 724
Db 1 TTGCGCTTTATCCCTCCCTCTCATTTGTTTAAATGATCGCTACCAACGGTGGAGTCCA 60
QY 725 AGCTCTACTCCATTGTTTGTGGAAATCGACACCTGAAAGAGAGGGGAGCTTTGAAGAA 784
Db 61 AGCTCTACTCCATTGTTTGTGGAAATCGACACCTGAAAGAGAGGGGAGCTTTGAAGAA 120
QY 785 CTACTACTAAGCCCTGGCCCAAAACCAAGCTTCAGTCCCACTCCAGGCTTCACCCCA 844
Db 121 CTACTACTAAGCCCTGGCCCAAAACCAAGCTTCAGTCCCACTCCAGGCTTCACCCCA 180
QY 845 CCCTGGGCTTCAGTCCGCTGCCAGTTCACCTTCACCTCCAGCTCCACCTATACCCCG 904
Db 181 CCCTGGGCTTCAGTCCGCTGCCAGTTCACCTTCACCTCCAGCTCCACCTATACCCCG 240
QY 905 GTGACTGTCCCAACTTTGGGCTCCCGCAGAGAGGTGGCACCCCTATCAGGGGGCTG 964
Db 241 GTGACTGTCCCAACTTTGGGCTCCCGCAGAGAGGTGGCACCCCTATCAGGGGGCTG 300
QY 965 ACCCATCTTTCGAGAGCCCTCGCTCGGACCCCAATCCCAACCCCTTCAGAGTGGG 1024
Db 301 ACCCATCTTTCGAGAGCCCTCGCTCGGACCCCAATCCCAACCCCTTCAGAGTGGG 360
QY 1025 AGGACAGCGCCACACAGCCACAGAGCTAGACACTGATGACCCCGGAGCTGTAGCGG 1084
Db 361 AGGACAGCGCCACACAGCCACAGAGCTAGACACTGATGACCCCGGAGCTGTAGCGG 420
QY 1085 TGGTGAGAACGTGCCCGGTTGCGCTGGAAGGAATTCGTGCGGGCCCTAGGGCTGAGG 1144
Db 421 TGGTGAGAACGTGCCCGGTTGCGCTGGAAGGAATTCGTGCGGGCCCTAGGGCTGAGG 480
QY 1145 ACCACGAGATCATCGCTGGAGCTGCAGACGGGGCTGCTGCGGAGGCGCAATACA 1204
Db 481 ACCACGAGATCATCGCTGGAGCTGCAGACGGGGCTGCTGCGGAGGCGCAATACA 540
QY 1205 GCATGCTGGGACCTGGAGCGGCGCACCGCGCGGCGGAGGCGCTGAGCTGCTGG 1264
Db 541 GCATGCTGGGACCTGGAGCGGCGCACCGCGCGGCGGAGGCGCTGAGCTGCTGG 600
QY 1265 GACGCTGCTCCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGAGGCGCTT 1324
Db 601 GACGCTGCTCCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGGAGGCGCTT 660
QY 1325 GGGGCGCGCGCGCTCCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1368
Db 661 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 703
```

```
RESULT 6
AUI31978
LOCUS AUI31978 NT2RP3 Homo sapiens cDNA clone NT2RP3003570 5', mRNA
DEFINITION sequence.
ACCESSION AUI31978
VERSION AUI31978.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 761)
Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y.,
Yamamoto.J., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and
Isogai.T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
```

```
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1..761
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT2RP3"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/notes="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT 178 a 199 c 201 g 179 t 4 others
ORIGIN
Query Match 49.9%; Score 682.4; DB 9; Length 761;
Best Local Similarity 99.1%; Pred. No. 6.1e-158;
Matches 694; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 1 ATGGGGCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGCTGCTGCTGCTGCTGCTG 60
Db 62 ATGGGGCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGCTGCTGCTGCTGCTGCTG 121
QY 61 GGAATATATACCTCAGGGGTTATTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 122 GGAATATATACCTCAGGGGTTATTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 181
QY 121 GATAGTGTCTGCTGCCCAAGAAATATATCCACCTCAAAATATATTCGATTTGCTG 180
Db 182 GATAGTGTCTGCTGCCCAAGAAATATATTCACCTCAAAATATATTCGATTTGCTG 241
QY 181 AAGTGCCACAAAGGACCTTACTTGTACAATGACTGTCCAGGGCGGGGAGGATACGGAC 240
Db 242 AAGTGCCACAAAGGACCTTACTTGTACAATGACTGTCCAGGGCGGGGAGGATACGGAC 301
QY 241 TGCAGGAGTGTGAGAGCGGCTCTTCCACCGCTTCAGAAACACCTCAGACACTGCCTC 300
Db 302 TGCAGGAGTGTGAGAGCGGCTCTTCCACCGCTTCAGAAACACCTCAGACACTGCCTC 361
QY 301 AGCTGCTCAAAATCGCGAAGAAATGGCTGAGTGGAGTCTCTTCTTCCACAGTGGAC 360
Db 362 AGCTGCTCAAAATCGCGAAGAAATGGGTGAGTGGAGTCTCTTCTTCCACAGTGGAC 421
QY 361 CGGGACACCGTGTGTGCTGCAGGAAGAACCACTACCGCATTTATTTGGAGTGAACCTT 420
Db 422 CGGGACACCGTGTGTGCTGCAGGAAGAACCACTACCGCATTTATTTGGAGTGAACCTT 481
QY 421 TTCCAGTGTCTCAATTCAGACCTCTGCTCAATTCAGGACCGTGCACCTCTCTCTGCCAGGAG 480
Db 482 TTCCAGTGTCTCAATTCAGACCTCTGCTCAATTCAGGACCGTGCACCTCTCTCTGCCAGGAG 541
QY 481 AAGACAGACACCGTGTGCACCTGCCATGAGGTTCTTTCTTCTAGAGAAACAGTGTCTC 540
Db 542 AAGACAGACACCGTGTGCACCTGCCATGAGGTTCTTTCTTCTAGAGAAACAGTGTCTC 601
QY 541 TCCTGTAGTAACCTGTAAGAAAGCCCTGGAGTGCAGCAAGTTGTGCTTACCCACAGATTGAG 600
Db 602 TNCGTGTAGTAACCTGTAAGAAAGCCCTGGAGTGCAGCAAGTTGTGCTTACCCACAGATTGAG 661
QY 601 AATGTTAAGGGCACTGAGGACTCAGCCACACAGTGC-TGTTGCCCTCGTCAATTTCTT 659
Db 662 AATGTTAAGGGCACTGAGGACTCAGGACCCAGCAATGCTTGTGCTGCTGCTGCTGCT 721
QY 660 TGGTCTTTGCTTTTATCCCTCTCTCTTCATTTGTTTAATG 699
Db 722 TGGTCTTTGCTTTTATCCCTNCTCTTCATTTGTTTAATG 761
```

FEATURES
source

Matches	741:	Conservative	0:	Mismatches	38:	Indels	9:	Gaps	3:
Qy	1	ATGGGCTCTCCACCGTGCCTGACTGCTGCTGCACCTGGTGTCTCTGGAGCTGTGGTG	60						
Db	206	ATGGGCTCTCCACCGTGCCTGACTGCTGCTGCCGCTGGTGTCTCTGGAGCTGTGGTG	265						
Qy	61	GGAAATACCCCTCAGGGGTATTGGACTGGTTCCTCACCTAGGGACAGGGGAGAAGGA	120						
Db	266	GGAAATACCCCTCAGGGGTATTGGACTGGTTCCTCACCTAGGGACAGGGGAGAAGGA	325						
Qy	121	GATAGTGTGTGCCCAAGGAAATATATCCACCTCAAAATTAATTCGATTTCGTGTACC	180						
Db	326	GATAGTGTGTGCCCAAGGAAATATATCCACCTCAAAATTAATTCGATTTCGTGTACC	385						
Qy	181	AAGTGCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC	24						
Db	386	AAGTGCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGAC	445						
Qy	241	TGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAACCACTTCAGACACTGCCTC	300						
Db	446	TGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAACCACTTCAGACACTGCCTC	505						
Qy	301	AGCTGCTCCAAATGCCGAAAGAAATGGGTCAAGTGGAGATCTCTTCTTGACACAGTGGAC	360						
Db	506	AGCTGCTCCAAATGCCGAAAGAAATGGGTCAAGTGGAGATCTCTTCTTGACACAGTGGAC	565						
Qy	361	CGGGACACCGTGTGTGGCTGCAGAGAACCAAGTACCGGCATTATTGGAGTGAACACTT	420						
Db	566	CGGGACACCGTGTGTGGCTGCAGAGAACCAAGTACCGGCATTATTGGAGTGAACACTT	625						
Qy	421	TTCCAGTGTCAATTGCACGCTCTGCTCAATGGGACCGTGCACCTCTCTGCCAGGAG	480						
Db	626	TTCCAGTGTGTCAATTGCACGCTCTGCTCAATGNGACCGTGCACCTCTCTGCCAGGAG	685						
Qy	481	AAACAGAACACCGTGTGCACCTGCCATGCAAGTTTCTTCTAAGAGAAAAACGAGTGTCT	540						
Db	686	AAACAGAACACCGTGTGCACCTGCCATGCAAGTTTCTTCTAAGAGAAAAACGAGTGTCT	745						
Qy	541	TCCTGTAGTAACCTGAAGAAAGCCTGGAGTGCACGAAGTGTGCCCTACCCAGATTGAG	600						
Db	746	TCCTGTAGTAACCTGAAGAAAGCCTGGAGTGCACGAAGTGTGCCCTACCCAGATTGAG	805						
Qy	601	AATGTTAAGGGCACTGAGGACTCAGGCACCACTGCTGTGTG - CCCCTGGTCTATTTCTT	659						
Db	806	AATGGTAAGGGCACTGAGGACTCAGGCACCACTGCTGTGTG - CCCCTGGTCTATTTCTT	865						
Qy	660	TGGTCTTTGGCTTTTATCCCTCTCTTCATTGGTTTAAATGTATCGCTTACCAAC - - GGTTG	717						
Db	866	TGGGCTTTGGCTTTTATCCCTCTCTTCATTGGTTTAAATGTATCGCTTACCAACCGGGTGG	925						
Qy	718	AAGTCCAAAG - - - - - CTCTACTCCATTGTTTGTGGGAAATCGACACCTGAAAAAGAGGG	771						
Db	926	AAGTCCCAAGGCTCTACCTCCCTGGTTTGGGGGGGAAATCCGACACCTTGGAAAAAGAGG	985						
Qy	772	GAGCTTGA	779						
Db	986	GGGGAAGA	993						

RESULT 9
AL577008
LOCUS
DEFINITION
AL577008 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1082YA01 5
975 bp mRNA linear EST 16-FEB-2001
prime, mRNA sequence.
ACCESSION
AL577008
VERSION
AL577008.1 GI:12939716
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 975)
REFERENCE
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES Location/Qualifiers
 1. 975
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0D1082YA01"
 /clone_lib="LTI_NFL006_PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site.1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies, Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"
 231 a 258 c 259 g 221 t 6 others
 BASE COUNT
 ORIGIN

Query Match	49.6%	Score 678.2	DB 9	Length 975
Best Local Similarity	97.9%	Pred. No. 6.9e-157		
Matches 704	Conservative 4	Mismatches 8	Indels 3	Gaps 2
Qy	1	ATGGGGCCTC	CCACCGTGCCTGACCTGCTGCTGCCACTGGTGCCTCGAGCTGTGCTCGAGCTGTGGTG	60
Db	256	ATGGGCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCCTCGAGCTGTGGTG	315	
Qy	61	GGAATATACCCCTC	CAGGGGTATTGGACTGTGCTCCTCACCTAGGGGACAGGGAAGAGA	120
Db	316	GGAATATACCCCTC	CAGGGGTATTGGACTGTGCTCCTCACCTAGGGGACAGGGAAGAGA	375
Qy	121	GATAGTGTGTG	TCCCCAAGGAAATATATCCACCTCAAAATAATTCGATTTCGTGTAC	180
Db	376	GATAGTGTGTG	TCCCCAAGGAAATATATCCACCTCAAAATAATTCGATTTCGTGTAC	435
Qy	181	AAGTGCCACA	AAAGAACCTACTTGTACAAACACTGTCAGGCCCGGGCAGGATACGAC	240
Db	436	AAGTGCCACA	AAAGAACCTACTTGTACAAACACTGTCAGGCCCGGGCAGGATACGAC	495
Qy	241	TGCAGGAGTGTG	AGAGCGGCTCCTTCCACCGCTTCAGAAAAACCACTCCAGACACTGCCCTC	300
Db	496	TGCAGGAGTGTG	AGAGCGGCTCCTTCCACCGCTTCAGAAAAACCACTCCAGACACTGCCCTC	555
Qy	301	AGCTGCTCCAAAT	CGCGAAAGGAAATGGGTGAGATCTCTTTCGACAGTGGAC	360
Db	556	AGCTGCTCCAAAT	CGCGAAAGGAAATGGGTGAGATCTCTTTCGACAGTGGAC	615
Qy	361	CGGACACCGTGTG	TGGCTGAGGAAGAACCACTACCGGCATATTGGAGTGAACCTT	420
Db	616	CGGACACCGTGTG	TGGCTGAGGAAGAACCACTACCGGCATATTGGAGTGAACCTT	675
Qy	421	TTCCAGTGTTC	CAATTCAGCCTCTGCTCAATGGGACCGTCACCTCTCCTGCCAGAG	480
Db	676	TTCCAGTGTTC	CAATTCAGCCTCTGCTCAATGGGACCGTCACCTCTCCTGCCAGAG	735
Qy	481	AAACAGAAC	ACCGTGTGCACCTGCATCAGGTTTCTTTTAAAGAAACAGGTGCTC	540
Db	736	AAACAGAAC	ACCGTGTGCACCTGCATCAGGTTTCTTTTAAAGAAACAGGTGCTC	795
Qy	541	TCCTGTAGT	AACTGTAAAGAAAGCCTGGAGTGCACGAAGTTG-TGCCCTACCCCGATTTGA	599
Db	796	TYCTGTAGT	AACTGTAGTAAAGAAAGCCTGGAGTGCACGAAGTTGSGTGCCTACCCAGATTGA	855
Qy	600	GAATGTTAAG	GGCACTAGGACTCAGGCCACACAGTGTGTGGCCCTGGTCAATTTCTT	659
Db	856	GAATGTTAAG	GGCACTAGGACTCAGGCCACACAGTGTGTGGCCCTGGTCAATTTCTT	915

JOURNAL
Tumor Gene Index
Unpublished (1997)

Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

The following repetitive elements were found in this cDNA through the I.M.A.G.E: Consortium/EMBL at: <http://image.jim.gov>

```

sequence: 669-696, >GC_rich#Low_complexity
Seq primer: M13 FORWARD

```

POLYA=Yes.
Location/Qualif for

source	1. .696
source	1. .696

```
/organism="Homo sapiens"  
/db_xref="taxon:9606"
```

```

/clone="IMAGE:5862208"
/clone lib="NCI CGAP D10"

```

```

/tissue_type="Lung Focal Fibrosis"
/dec stnco="adult"

```

```

/lab_host="DH10B (Life Technologies)"

```

```

/note--Organ: Lung; vector: pT/T3-PAC (Pharmacia), with
modified polylinker; Site_1: EcoR I; Site_2: Not I;

```

NCI_CGAP_D10 is a cDNA library containing the following tissue(s): A pool of Lung Focal Fibrosis. The library was

constructed according to Bonaldo, Lennon and Soares, Genome Research 6:701-806 1996 first strand cDNA

synthesis was primed with an oligo-dT primer containing

NOT I site. Double stranded cDNA was ligated to an EcoR adaptor, digested with Not I, and cloned directionally

into pT7T3-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library t

sequence that is located between the Not I site and the

(AT)25 CAT. The sequence tag for this library is ATACCGGTC.

TAG_LIB=UI-R-DIV
 TAG_TISSUE=lung with fibrosis

TAG_SEQ-ATACGGGTC ^W		
BASE COUNT	128 a	244 c
	132 t	2 others

ORIGIN

Query Match	48.8%	Score 667.8;	DB 14;	Length 696;
-------------	-------	--------------	--------	-------------

Best Local Similarity 98.0%; Fied. NO. 2.4E-134;
Matches 675; Conservative 0; Mismatches 14; Indels 0; Gaps

658 TTTGGTCTTTGCCCTTTATCCCTCCTCTTCATTGGTTTAA TGTATCGGTACCAACGGTGG 7

[illegible][illegible]

QY /18 AAGTCCAAAGCTCTACTCCATTGTTTGTGTGGAAATCGACACCCTGAAAAAGAGGGGAGCTT

62 AAGTCCAAGCTCTACTCTCATTTGTTGTGGGAAATCGACACCTGAAAAGAGGGGAGCTT 1

QY 778 GAAGGAAC TACTACTA AGCCCTG GCGCCCA ACCCAAG CTTCAGT CCCTC CACTC CAGGCTC 8

Db 122 GAAGGACTACTAAGCCCTGGCCCAACCAAGCTTCAGTCCCTCAGGCTTC 18

QY 838 ACCCCACCCCTGGGCTTCAGTCCCGTGCCCGAGTTCACCTCCAGCTCCACCTAT 8

1

Db 182 ACCCCCCACCCCTTGCAGTCCCTGCGCCAGTTCACCTTCCACCTTCCACCTCCAGCTCCACCTAT 241
QY 898 ACCCCCGGTGACTGTCCTCAACTTTTGGCGCTCCCGCAGAGAGTGGCACCCTTATCAG 957
Db 242 ACCCCCGGTGACTGTCCTCAACTTTTGGCGCTCCCGCAGAGAGTGGCACCCTTATCAG 301
QY 958 GGGGCTGACCCATCCTTTGGACAGCCTTGGCTCCGACCCATCCCAACCCCTTCCAG 1017
Db 302 GGGGCTGACCCATCCTTTGGACAGCCTTGGCTCCGACCCATCCCAACCCCTTCCAG 361
QY 1018 AAGTGGGAGGACAGCGCCACAGCCACAGAGCTTAGACCTGATGACCCCGGACGCTG 1077
Db 362 AAGTGGGAGGACAGCGCCACAGCCACAGAGCTTAGACCTGATGACCCCGGACGCTG 421
QY 1078 TACGCGGTGGTGGAGAGCTGCCCCGCTGGCTGGAAGGAATTCGTGGCGCGCTAGGG 1137
Db 422 TACGCGGTGGTGGAGAGCTGCCCCGCTGGCTGGAAGGAATTCGTGGCGCGCTATGG 481
QY 1138 CTGAGCGACACAGAGATCGATGGCTGGAGCTGCAGAACCGCGCGCTGCTCGCGAGCG 1197
Db 482 CTGAGCGACACAGAGATCGATGGCTGGAGCTGCAGAACCGCGCGCTGCTCGCGAGCG 541
QY 1198 CAATACACATGCTGGCGACCTGGAGCGCGCAGCGCGCGCGCGCGCGCGCGCGCG 1257
Db 542 CAATACACATGCTGGCGACCTGGAGCGCGCAGCGCGCGCGCGCGCGCGCGCGCG 601
QY 1258 CTGCTGGGACGCTGCTCCGCGACATGACCTGCTGGCTGGCTGGAGGACATCGAGGAG 1317
Db 602 CTGCTGGGACGCTGCTCCGCGACATGACCTGCTGGCTGGCTGGAGGACATCGAGGAG 661
QY 1318 GCGCTTGGCGCGCGCGCGCGCGCTCCGCGC 1346
Db 662 GCGCTTGGCGCGCGCGCGCGCGCTCCGCGC 690

RESULT 13

LOCUS BG680679
DEFINITION 602626965F1 NCI_CGAP_Skn4 Homo sapiens cdna clone IMAGE:4751536 5',
mRNA sequence.

ACCESSION BG680679

VERSION BG680679.1 GI:13912076

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 718)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLNL0608 row: b column: 17

High quality sequence stop: 679.

Location/Qualifiers

1..718

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4751536"

/lab_host="DH10B (T1 phage-resistant)"

/tissue_type="squamous cell carcinoma"

/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1; NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.5kb. Library constructed by Life

FEATURES

source

BASE COUNT 134 a 254 c 198 g 132 t
ORIGIN

Query Match 48.8%; Score 667; DB 12; Length 718;

Best Local Similarity 98.4%; Pred. No. 3.8e-154;

Matches 684; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 654 TTTCTTTGGCTTTGGCTTTTATCCCTCTCTTCTTATGTTGTTTAAATGATTCCTACCAACG 713

Db 1 TTTCTTTGGCTTTGGCTTTTATCCCTCTCTTCTTATGTTTAAATGATTCCTACCAACG 60

QY 714 GTGAAGTCCAAGCTTACTTCCATTTTGTGGAAATCGACACTGAAAAAGAGGGGA 773

Db 61 GTGAAGTCCAAGCTTACTTCCATTTTGTGGAAATCGACACTGAAAAAGAGGGGA 120

QY 774 CTTGAAGAACTACTACTAAGCCCTGGCCCAAAACCAAGCTTCAGTCCCATCCAGG 833

Db 121 CTTGAAGAACTACTACTAAGCCCTGGCCCAAAACCAAGCTTCAGTCCCATCCAGG 180

QY 834 CTTACACCCCACTGGGCTTCAGTCCGTCGCCAGTTCACCTTCACCTCCAGCTCCAC 893

Db 181 CTTACACCCCACTGGGCTTCAGTCCGTCGCCAGTTCACCTTCACCTCCAGCTCCAC 240

QY 894 CTATACCCCGGTGACTGTCCCAACTTTTGGCGCTCCCGCAGAGAGTGGCACCACCTA 953

Db 241 CTATACCCCGGTGACTGTCCCAACTTTTGGCGCTCCCGCAGAGAGTGGCACCACCTA 300

QY 954 TCAGGGGGCTACCCCATCTTGGACAGCCCTGCGCTCCGACCCCATCCCCACCCCT 1013

Db 301 TCAGGGGGCTACCCCATCTTGGACAGCCCTGCGCTCCGACCCCATCCCCACCCCT 360

QY 1014 TCAGAAGTGGGAGGACAGCGCCACAAAGCCACAGAGCTAGTATGATGACCCCGGAC 1073

Db 361 TCAGAAGTGGGAGGACAGCGCCACAAAGCCACAGAGCTAGTATGATGACCCCGGAC 420

QY 1074 GCTGTACGCCCTGGTGGAGAACGTGCCCGCTTGGCTGGAGGAATTCGTGCGCGCGCT 1133

Db 421 GCTGTACGCCCTGGTGGAGAACGTGCCCGCTTGGCTGGAGGAATTCGTGCGCGCGCT 480

QY 1134 AGGCTGAGCGGACACAGATCGATCGGCTGAGCTGCAGAACCGGCGCTGCTGCGCGGA 1193

Db 481 AGGCTGAGCGGACACAGATCGATCGGCTGAGCTGCAGAACCGGCGCTGCTGCGCGGA 540

QY 1194 GGCCTAATACAGTCTGTCGAGCTGGAGCGCGCAGCGCGCGCGCGCGCGCGCGCT 1253

Db 541 GGCCTAATACAGTCTGTCGAGCTGGAGCGCGCAGCGCGCGCGCGCGCGCGCGCT 600

QY 1254 GGAGCTGCTGGAGCGCTGCTCCCGGACATGGAGCTGCTGGCTGCTGGAGG-ACATCG 1312

Db 601 GGAGCTGCTGGAGCGCTGCTCCCGGACATGGAGCTGCTGGCTGCTGGAGGACATCG 660

QY 1313 AGGAGGCGCTTGGCGGCGCGCGCGCGCTCCCGCGCC 1347

Db 661 AGGAGGCGCTTGGCGGCGCGCGCGCGCTCCCGCGCC 695

RESULT 14
LOCUS BM800044
DEFINITION AGENCOURT_6415909 NIH_MGC_71 Homo sapiens cdna clone IMAGE:5531041
5', mRNA sequence.

ACCESSION BM800044

VERSION BM800044.1 GI:19116867

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 994)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)


```
Db 438 TGCAGGGAGTGTGAGAGCGGCTCCTTACCGCTTCAGAAACCACCTCAGACACTGCCTC 497
QY 301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAAGGTGGAGATCTTCTTTCACACAGTGGAC 360
Db 498 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAAGGTGGAGATCTTCTTTCACACAGTGGAC 557
QY 361 CGGGACACCGTGTGTGGCTGAGGAAGAACCCAGTACCGGCATTATTGGAGTGAACCTT 420
Db 558 CGGGACACCGTGTGTGGCTGAGGAAGAACCCAGTACCGGCATTATTGGAGTGAACCTT 617
QY 421 TTCCAGTCTTCAATTGACGCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
Db 618 TTCCAGTCTTCAATTGACGCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 677
QY 481 AAACAGAACACCGTGTGCACCTGCGCATGCAAGTTTCTTCTAAGAGAAACGAGTGTGTC 540
Db 678 AAACAGAACACCGTGTGCACCTGCGCATGCAAGTTTCTTCTAAGAGAAACGAGTGTGTC 737
QY 541 TCCTGTAGTAACGTGAAGAAAGCCTGGAGTGCACGAAGTTGTGCTTACCCAGATTGAG 600
Db 738 TCCTGTAGTAACGTGAAGAAAGCCTGGAGTGCACGAAGTTGTGCTTACCCAGATTGAG 797
QY 601 AATGTTAAGGGCACTGAGGACTCAGGCACACAGTGTGT 640
Db 798 AATGTTAAGGGCACTGAGGACTCAGGCACACAGTGTGT 837
```

Search completed: June 9, 2003, 00:13:31
Job time : 1870 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein : nucleic search, using frame_plus_p2n model

Run on: June 8, 2003, 23:42:19 ; Search time 299 Seconds
(without alignments)
3426.954 Million cell updates/sec

Title: US-09-899-422a-2

Perfect score: 2487

Sequence: 1 MGLSTVPDLLPLVLELLV.....DIEELCGPAALPPAPSLLR 455

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool/US09899422/runat_04062003_145736_14694/app_query.fasta_1.647
-DB=N_Geneseq_101002 -OPMT=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09899422.ecgn_1.1_396.ernat_04062003_145736_14694 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_101002.*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2487	100.0	1368	14	AAQ49932	Lambda-derived TNF
2	2487	100.0	1368	21	AAA95105	Human TNFR1 coding
3	2487	100.0	2062	13	AAQ20973	TNF-alpha binding
4	2487	100.0	2062	13	AAQ24440	Encodes TNF-alpha
5	2487	100.0	2088	12	AAQ10883	30kD TNF inhibitor
6	2487	100.0	2088	22	AAQ83946	Human 30 kDa TNF 1
7	2487	100.0	2111	20	AAQ209170	Human tumour necro
8	2487	100.0	2111	22	AAH48859	Human TNFBP-associ
9	2487	100.0	2111	24	ABK84039	Human CDNA differe
10	2487	100.0	2111	24	ABN95862	Gene #2360 used to
11	2487	100.0	2161	21	AAZ48475	Human tumour necro
12	2487	100.0	2161	24	ABK13194	Human tumour necro
13	2487	100.0	2175	16	AAQ90513	p55 TNF-R gene. H
14	2484	99.9	2111	12	AAQ10955	Encodes human 55kD
15	2478	99.6	2170	14	AAQ50870	p55 Tumour necrosi
16	2471	99.4	2141	11	AAQ06285	Human Tumour Necro
17	2464	99.1	2176	12	AAQ12215	Type I TNF recepto
18	2069	83.2	1334	14	AAQ6282	Plasimid Tumour Nec
19	1563.5	62.9	2130	24	ABK63694	Rat sequence diffe
20	1539.5	61.9	2173	11	AAQ06284	Rat Tumour Necrosi
21	1223.5	49.2	6889	17	AAV15931	DHFR/Inttron (WTra
22	1213.5	48.8	2254	21	AAQ95104	Partial human TNFR
23	1192	47.9	6926	18	AAV04431	Vector pCDNA3-IgG1
24	1130	45.4	608	13	AAQ24441	Encodes truncated
25	1016	40.9	1301	18	AAQ94022	CDNA for TBP(20-19
26	995.5	40.0	1147	18	AAQ94021	CDNA for TBP(20-19
27	992	39.9	1478	20	AAQ58150	CadC-fusion polype
28	946	38.0	504	13	AAQ24445	Encodes truncated
29	941	37.8	483	19	AAV15468	Human soluble tumo
30	941	37.8	483	19	AAV19801	Soluble tumour nec
31	941	37.8	483	20	AAV81732	Tumour necrosis in
32	941	37.8	483	20	AAV81732	Human 30 kDa TNF 1
33	870.5	35.0	1202	18	AAQ94008	CDNA for TBP(20-16
34	854.5	34.4	477	13	AAQ24444	Encodes truncated
35	852	34.3	1049	18	AAQ94007	CDNA for TBP(20-16
36	840	33.8	462	13	AAQ24443	Encodes truncated
37	840	33.8	474	13	AAQ24442	Encodes truncated
38	809	32.5	1358	21	AAA95103	Partial human TNFR
39	790	31.8	507	24	ABL99490	Target canine gene
40	767.5	30.9	1977	24	ABA99913	TNF-selectokine pr
41	766.5	30.8	5870	21	AAV15044	Nucleotide sequenc
42	756.5	30.4	1674	21	AAV50196	Male fusion plasm
43	638	25.7	339	19	AAV19804	Truncated stNFR, s
44	621	25.0	333	19	AAV19805	Truncated stNFR, s
45	615	24.7	332	19	AAV19803	Truncated stNFR, s

ALIGNMENTS

RESULT 1

AAQ49932

ID AAQ49932 standard; CDNA to mRNA; 1368 BP.

XX AC AAQ49932;

XX DT 29-APR-1994 (first entry)

XX DE Lambda-derived TNF-R CDNA.

XX KW Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
XX KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
XX KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
XX KW graft versus host disease; sepsis; inflammation; allergy;
XX KW autoimmune dysfunction; ss.
XX OS Homo sapiens.

OS Lambda-gt10-7-ctnfbp.
 XX Key Location/Qualifiers
 FH CDS 1..1366
 FT /*tag= a
 FT /product= hTNF-R
 FT sig_peptide 1..120
 FT mat_peptide 121..1363
 FT /*tag= b
 FT /*tag= c
 XX WO9319777-A.
 XX 14-OCT-1993.
 XX 26-MAR-1993; 93WO-US02938.
 XX 30-MAR-1992; 92US-0860710.
 XX (IMMV) IMMUNEX CORP.
 XX Smith CA;
 XX WPI: 1993-336592/42.
 XX P-PSDB; AAR42059.
 XX New fusion protein tumour necrosis factor and human interleukin-1
 PT receptor - useful in therapy, diagnosis and assays of e.g.
 PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
 PS Disclosure; Page 57-59; 85pp; English.
 XX The sequences given in AAQ49931-32 encode human tumour necrosis factor
 CC receptor (TNF-R) and the sequences in AAQ49933-34 encode human
 CC interleukin-1 receptor (IL-1R). These sequences were used in the
 CC production of a fusion protein which conformed to one of the
 CC formulae:
 CC TNF-R-linker-TNF-R-linker-IL-1R
 CC IL-1R-linker-TNF-R-linker-TNF-R or
 CC TNF-R-linker-TNF-R
 CC The linker may comprise 5-100 amino acids selected from Gly, Asp,
 CC Ser, Thr and Ala. These linkers separate the individual moieties
 CC by such a distance that each component of the fusion protein is
 CC capable of folding into the secondary or tertiary structure required
 CC for its biological activity. These fusion proteins may be used in
 CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
 CC particularly in conditions in which both TNF and IL-1 play a causative
 CC role. They may be used to treat cachexia, rheumatoid arthritis,
 CC diabetes, multiple sclerosis, pulmonary fibrosis and atherosclerosis,
 CC cerebral malaria, allograft and xenograft rejection in graft versus
 CC host disease, sepsis, septic shock, inflammation, allergies and
 CC autoimmune dysfunctions.
 XX Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T; 0 other;
 SQ

Alignment Scores:
 Pred. No.: 1,72e-174 Length: 1368
 Score: 2487.00 Matches: 455
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-09-899-422a-2 (1-455) x AAQ49932 (1-1368)

Qy 1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuLeuVal 20
 DB 1 ATGGGCGCTCTCCACCGTGCCTGACCTGCTGCTGCGCTGGTGGTCTGCTGGAGCTGTGGTG 60
 Qy 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluIysArg 40
 DB 61 GGATATACCCCTCAGGGGTATTGGACTGTGCTCCCTCACCCTAGGGGACAGGAGAGAGA 120

QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
 DB 121 GATAGTGTGTGCCCCAAGAAAAATATATCCACCCTCAAAATAATTCGATTTCGTGTACC 180
 QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyClnAspPhrAsp 80
 DB 181 AAGTCCCAAAAGGAACCTACTTGTACAAATGCTCCAGGCGCCGGGCGAGATACGGAC 240
 QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
 DB 241 TGCAGGGAGTGTGACAGCGGCTCCTTACCGCTTCAGAAACCACCTCAGACACTGCCUC 300
 QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
 DB 301 AGCTGCTCCAAATGCCAAAGGAAATGGTCAAGTGGAGATCTCTTCTTGCACAGTGGAC 360
 QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
 DB 361 CGGGACACCGTGTGTGGCTGCGAGGAACCACTGACCGCTTCAGAAACCACCTCAGACACTGCCUC 420
 QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
 DB 421 TTCCAGTGTTCATTTGACGCTCTGCCTCAATGGGACCGTGCACCTCTCTGCGCAGGAG 480
 QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
 DB 481 AAACAGAACACCGTGTGCACCTGCCATCGAGTTTCTTTTCTAAGAGAAACAGTGTGTC 540
 QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
 DB 541 TCTGTAGTAACTGTAAAGAAAGCCTGGAGTGCACGAAGTTGTGCTTACCCAGATTGAG 600
 QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
 DB 601 AATGTTAAGGCACCTGAGGACTCAGSCACACAGTGTCTTGGCCCTGCTCATTTCTTT 660
 QY 221 GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
 DB 661 GGTCTTTGCTTTTATCCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 720
 QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGluLeuGlu 260
 DB 721 TCCAGCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
 QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
 DB 781 GGAACCTACTTAAGCCCTTGCCGCCCAACCAACCAAGCTTCACTGCCACTCCAGCTTACC 840
 QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300
 DB 841 CCCACCTTGGGCTTTCAGTCCCGTGCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 900
 QY 301 ProGlyAspCysProAsnPheAlaProArgGluValAlaProProTyrGlnGly 320
 DB 901 CCCGTTGACTTCCCACTTTGCGGCTCCCCGACAGAGGTGGACCACTTATCAGGGG 960
 QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
 DB 961 GCTGACCCCATCTCTTGCAGACAGCCCTCGCTCCGACCCCACTCCCAACCCCTTCCAGAG 1020
 QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
 DB 1021 TGGGAGGACAGCGCCACCAAGCCACAGACCTAGACACTGTAGCCCGCGCAGCTGTAC 1080
 QY 361 AlaValValGluAsnValProLeuArgTrpLysGluPheValArgArgLeuGlyLeu 380
 DB 1081 GCCGTGGTGGAGAGCTGCCCTTGTGCGTGGAGGAATTCGTGCGCGGCTTACGGGTG 1140
 QY 381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
 DB 1141 AGCGACACAGAGATCGATCGCTGGAGCTGCAGAACGGCGCTGCTCGCGGAGCGGCA 1200
 QY 401 TyrSerMetLeuAlaThrTrpArgArgThrProArgGluAlaThrLeuGluLeu 420

QY 41 AspSerValCysProGlnGlyTyrThrLeuHisProGlnAsnAsnSerIleCysCysThr 60
DB 275 CATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATATTCGATTGTGTATCC 334
QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlnAspThrAsp 80
DB 335 AAGTCCCAACAAGGAACCTACTTGTACATGACTGTCCAGGCCCGGGCAGGATACGAC 394
QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
DB 395 TCCAGGGAGTGTGAGAGGGCTCTTCCACCGCTTCAGAAACACCACTCAGACACTGCCTC 454
QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
DB 455 AGCTGCTCCAAATGCCGAAGAAATGGTCAAGTGGAGATCTCTTCTGCACAGTGGAC 514
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
DB 515 CGGGACACCGTGTGTGGCTGCAGGAAGAACCACTACCGCATTTATGGAGTGAAACCTT 574
QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
DB 575 TTCCAGTCTCAATGTGACCTCTGCTCAATGGACCGTGCACCTCTCTCTGCCAGGAG 634
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
DB 635 AAACAGACACCGTGTGCACCTGCCTCAGGCTTTCTTCTAAGAAACAGAGTGTGC 694
QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
DB 695 TCCTGTAGTAAGTAAGAAAGCTGGAGTGCAGCAAGTGTGTCTACCCAGATTGAG 754
QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhephe 220
DB 755 AATGTTAAGGGCACTGAGCACTCAGGACCACTGCTGTGCTGCCCTGCTCATTTTCTTT 814
QY 221 GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
DB 815 GGTCTTTGCTTTTATCCCTCTCTCATGTGTTTAAATGTATCGTACCAACGGTGGAG 874
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu 260
DB 875 TCCAAGCTACTTCCATTTGTTGGAAATCGACACCTGAAAGAGGGGAGGTTGAA 934
QY 261 GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
DB 935 GGAACCTACTTAAGCCCTGCGCCCAACCAAGCTTCAGTCCCACTCCAGGCTTCACC 994
QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrThrThr 300
DB 995 CCCACCTGGGCTTCAGTCCCTGCGCCAGTTCACCTTCACCTCCAGCTCCACCTATACC 1054
QY 301 ProGlyAspCysProAsnPheAlaAlaProArgGluValAlaProProTyrGlnGly 320
DB 1055 CCCGTTGACTGTCCCAACTTTGCGCTCCCGCAGAGGTGGCACCCTATCAGGGG 1114
QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
DB 1115 GCTGACCCCATCTTGTGCGACAGCCCTGCGCTCCGACCCCAACCCCTTCAGAAAG 1174
QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
DB 1175 TGGGAGGACAGTGGCCACAGCCACAGACCTTAGACACTGTAGCCCCCGCAGCTGTAC 1234
QY 361 AlaValValGluAsnValProProLeuArgTyrTrpLysGluPheValArgArgLeuGlyLeu 380
DB 1235 GCGTGTGTGGAACGTGCCCCGTGTGCTGGAAGGAATTCGTGGGGCCCTAGGGCTG 1294
QY 381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
DB 1295 AGCGACCAAGAGATCGATCGCTGGAGCTGCAGAACGGGCGCTGCTGCCGAGGGCCAA 1354
QY 401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420

DB 1355 TACACATGCTGGCGACCTGGAGCGGCGACGCGCGGCGGCGGCGGCGGCGGCTGAGCTG 1414
QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla 440
DB 1415 CTGGGACGGTGTCTCCGCGACATGACCTGCTGGGCTGCTGGAGACATCCAGGAGCG 1474
QY 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
DB 1475 CTTTGGCGCGCGCGCTCCCGCGCGCGCGCGCGCTCTTCTCAGA 1519
RESULT 4
AAQ24440
ID AAQ24440 standard; DNA; 2062 BP.
XX
AC AAQ24440;
XX
DT 05-NOV-1992 (first entry)
XX
DE Encodes TNF-alpha 55KD receptor.
XX
KW tumour necrosis factor alpha; extracellular binding domain;
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW malaria; viral meningitis; graft versus host disease;
KW autoimmune disease; rheumatoid arthritis.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 156..1517
FT /*tag= a.
FT /product= human TNF-alpha
FT mat_peptide 1265..1267
FT /*tag= b
FT /*note= "3"
FT mat_peptide 1265..1267
FT /*tag= c
FT /*codon= seq:"TGG", aa:Thr
FT mat_peptide 1258..1260
FT /*tag= d
FT /*codon= Seq"AAG", aa:Leu
FT mat_peptide 1433..1435
FT /*tag= e
FT /*codon= Seq:"GAC", aa:Asn
FT sig_peptide 156..274
FT /*tag= f
XX
PN WO207076-A.
XX
PD 30-APR-1992.
XX
PF 18-OCT-1991; 91WO-GB01826.
XX
PR 18-OCT-1990; 90GB-0022648.
XX
PA (CHAR-) CHARING CROSS SUNLEY RES CENT.
XX
PI Brennan FM, Feldmann M, Gray PW, Turner MJC;
XX
DR WPI: 1992-167156/20.
DR P-PSDB; AAR24000.
XX
PT New polypeptide capable of binding human TNF alpha - comprises
PT first three cysteine-rich subdomains of TNF alpha receptor for
PT treating autoimmune disease, septic shock, HIV etc.
XX
PS Claim 4; Fig 1: 43pp; English.
XX
CC This sequence encodes human TNF-alpha 55kd receptor . A placenta cDNA
CC library in gt10 was screened with probe AAQ29236. Ten hybridising clones
CC were plaque purified and cDNA size determined by PAGE against an
CC Eco RI digested phage DNA. The inserts of two cDNA clones were then
CC sequenced. The coding region of the majority of the human TNF-alpha

RESULT 8	
AAH48859	
ID	AAH48859 standard; DNA; 2111 BP.
XX	
AC	AAH48859;
XX	
DT	12-NOV-2001 (first entry)
XX	
DE	Human TNFBP-associated DNA #1.
XX	
TNF	TNF; tumor necrosis factor binding protein; TNFBP; treatment;
KW	insoluble protein; antinflammatory; immunosuppressive; antibacterial;
KW	antiprotoczoal; treatment; meningococcal sepsis; cerebral malaria;
KW	autolimmune glomerulonephritis; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	187..1554
FT	/*tag= a
FT	/product= "TNFBP-associated protein"
FT	187..270
FT	/*tag= b
FT	mat_peptide
FT	271..1551
FT	/*tag= c
XX	
PN	EPI132471-A2.
XX	
PD	12-SEP-2001.
XX	
PF	31-AUG-1990; 2001EP-0108117.
XX	
PR	12-SEP-1989; 89CH-0003319.
PR	08-MAR-1990; 90CH-0000746.
PR	20-APR-1990; 90CH-0001347.
PR	31-AUG-1990; 90EP-0116707.
PR	31-AUG-1990; 93EP-0100703.
XX	
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.
XX	
PI	Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
PI	Schlaeger E;
XX	
DR	WPI; 2001-559312/63.
DR	P-PSDB; AAB86817.
XX	
PT	New homogeneous, insoluble proteins that bind tumor necrosis factor
PT	(TNF), usefull for treating TNF-mediated disorders, e.g. inflammation
XX	
PS	Claim 4a; Fig 1; 26pp; German.
XX	
CC	This invention describes novel insoluble proteins (I), also their
CC	(In)soluble fragments and pharmaceutically acceptable salts, able to bind
CC	tumor necrosis factor (TNF) and in homogeneous form. The products of the
CC	invention have antinflammatory, immunosuppressive, antibacterial,
CC	antiprotoczoal activity. (I), and related recombinant proteins, are used
CC	to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
CC	sepsis; development of autoimmune glomerulonephritis and cerebral
CC	malaria. Also (I), or antibodies specific for them, are used for
CC	diagnostic determination of TNF in body fluids, for affinity purification
CC	of TNF and for identifying (ant)agonists of TNF. This sequence encodes a
CC	human TNF binding protein described in the method of the invention.
XX	
SQ	Sequence 2111 BP; 447 A; 627 C; 587 G; 450 T; 0 other;
XX	
Alignment Scores:	
Pred. No.:	3e-174
Score:	2487.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
Indels:	22
Gaps:	0
Length:	2111
Matches:	455
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

QY	121	ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu	140
DB	547	CGGGACACCGTGTGTGGCTGCAGAGAAACACAGTACCGCATTTATTGGAGTGAACACCTT	606
QY	141	PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu	160
DB	607	TTCACGATGCTCAATATGACGCTCTGCCTCAATGGACCGTGCACCTTCCTGCCAGGAG	666
QY	161	LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal	180
DB	667	AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTAAGAGAAAACGAGTGTGC	726
QY	181	SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu	200
DB	727	TCCTGTAGTAACGTGAAGAAAGCCGTGGAGTCACGAAAGTGTGTCCATACCCAGATTGAG	786
QY	201	AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe	220
DB	787	AAATGTTAAGGGCACTGAGGACTCAGGCACACAGTGTGTGTGCCCTGGTCAATTTCTTT	846
QY	221	GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTyrLys	240
DB	847	GGTCTTTGGCTTTTATCCCTCCTCTTCATTTGGTTTAAATGTATCGCTACCAACCGTGGAG	906
QY	241	SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeuLeuGlu	260
DB	907	TCCAAGCTCTACTCCATTGTTTGGGAAATGACACCTGAAAAAGAGGGGGAGCTTGAA	966
QY	261	GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr	280
DB	967	GGAACTACTACTAAGCCCTTGGCCCCAAACCCAAAGCTTCAGTCCCACTCCAGGCTTCACC	1026
QY	281	ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr	300
DB	1027	CCACACCTGGGCTTCAGTCCGCTGCCAGTTCACCTTCACCTCCAGCTCCACCTATACC	1086
QY	301	ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly	320
DB	1087	CCCGGTGACTGTCCCAACTTTGGCGCTCCCGCAGAGAGGTGGCACCCACCTATCAGGGG	1146
QY	321	AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys	340
DB	1147	GCTGACCCCATCTTGGCAGACGCGCTCGCTCCGACCCCATCCCAACCCCTTCAGAAG	1206
QY	341	TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr	360
DB	1207	TGGAGGACAGCGCCCAACAGCCACAGAGCTTAGACACTGATGCCCGCGAGCGCTGTAC	1266
QY	361	AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgLeuGlyLeu	380
DB	1267	GCGTGTGTGAGAAGCTGCCCGCTTGGCTGGAGGAATTCGTGGCGGCCCTTAGGGCTG	1326
QY	381	SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln	400
DB	1327	AGGCACACAGATCATCGCTGGAGCTGCAGAACCGGCGCTGCCGTGCCGAGGCGCAA	1386
QY	401	TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu	420
DB	1387	TACAGCATGTGGCGACTGGAGGCGGCACCGCGGGCGAGGCCAGCGCTGGAGCTG	1446
QY	421	LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla	440
DB	1447	CTGGGACCGCTGTCCCGACATGGAGCTGCTGGGCTGCTGGAGGACATCGAGGAGCGG	1506
QY	441	LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg	455
DB	1507	CTTTGGCGCGCGCGCCCTCCGCGCGCGCCAGTCTTCTCAGA	1551
RESULT 11			
AAZ48475			
ID AAZ48475 standard; DNA; 2161 BP.			
XX			

AC	AAZ48475;
DT	31-MAR-2000 (first entry)
XX	Human tumour necrosis factor receptor (TNFR1) nucleotide sequence.
DE	Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
XX	Inflammation; tumour formation; TNFR1; anticancer; ds.
KW	
KW	
OS	Homo sapiens.
XX	
XX	US6007995-A.
PB	28-DEC-1999.
XX	
PF	26-JUN-1998; 98US-0106038.
XX	
PR	26-JUN-1998; 98US-0106038.
XX	(ISIS-) ISIS PHARM INC.
PA	Baker BF, Cowse LM;
PI	WIPO; 2000-1053333/09.
XX	
DR	
PT	Antisense inhibition of tumor necrosis factor type 1 expression for
PT	diagnosis, treatment and prevention of disease, particularly tumors -
XX	
PS	Example 10; Columns 33-36; 34pp; English.
XX	The invention provides antisense compounds targeted to human tumour
CC	necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds
CC	can be used in a method of inhibiting the expression of TNFR1 human cells
CC	or tissues. The antisense compounds specifically hybridize with one or
CC	more nucleic acids encoding TNFR1 modulating the function of nucleic
CC	acid molecules encoding TNFR1, ultimately modulating the amount of TNFR1
CC	produced. The antisense compounds and method are useful as research
CC	reagents and diagnostics, and in the treatment and prophylaxis of
CC	infection, inflammation or tumour formation. The present sequence
CC	represents the nucleotide sequence of human TNFR1 (GenBank Accn No:
CC	X55313).
XX	
SQ	Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;
 Alignment Scores:	
Pred. No.:	3.le-174 Length: 2161
Score:	2487.00 Matches: 455
Percent Similarity:	100.00% Conservatative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	21 Gaps: 0
 US-09-899-422A-2 (1-455) x AAZ48475 (1-2161)	
Qy	1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuGluLeuVal 20
Dd	256 ATGGCGCTTCCACCCTGCCTGACTGCTGCTGCCGTGGTGCTCTCGAGCTTGGTG 315
Qy	21 GlyIleTyProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluYlYArg 40
Dd	316 GGAATATACCCCTCAGGGGGTTATTGGACTGTGGCTCACCTAGGGGACAGGAGAAGA 375
Qy	41 AspSerValCysProGlnGlyLysTyrlleHisProGlnAsnAsnSerIlleCysCysThr 60
Dd	376 GATAGTGTGTGTCCTCCCAAGAAAATAATATCCACCCTCAAATAATTCATTGCTGTACC 435
Qy	61 LysCysHisLysGlyThrTyrlleTyAsnAspCysProGlyProGlyGlnAspThrAsp 80
Dd	436 AAGTGCACAAGAACCTACTTGTACATGACTGTCCAGGCCCGGGGCAGCATACGGAC 495
Qy	81 CysArgGlnCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Dd	496 TGcAGGAGTGTcAGAGCGGCTCTTTCACCGCTTCAGAAACACCTCAGACACTGGCTC 555

RESULT 11
AAZ48475
ID AAZ4
XX

101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValasp 120
 556 AGCTGCTCCAAATCCCGAAGAAATGGTCAGGTGGAGATCTCTTTCACAGTGGAC 615
 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
 616 CGGACACCGGTGTGGCTGCAGAGAAACAGTACCGGCATTATTGGAGTGAACCTT 675
 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
 676 TTCAGTGTCTCAATTCAGACCTCTGCTCTCAATGGGACCGTGCACCTCTCTCCAGGAG 735
 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
 736 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTCTTCTAAGAGAAACAGAGTGTGC 795
 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
 796 TCTGTGTAGTAACCTGTGAAGAAAGCCCTGGAGTGCAGGAAGTTGTGCTACCCAGATTGAG 855
 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
 856 AATGTTAAGGCACTAGGACNCTCAGCACACAGTCTGTGCCCTGTGCATTTCTTT 915
 221 GlyLeuCysLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
 916 GGTCTTTTGCCTTTTATCCCTCTCTTCATTGTTTAAATGCTATCGCTACCAACGGTGGAG 975
 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGlnGlyGluLeuGlu 260
 976 TCCAGCTCTACTCCATTGTTGTGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 1035
 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
 1036 GGACTACTACTAAGCCCTGCCCCAACCAGCTTCAGTCCCACTCCAGGCTCAC 1095
 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrThrThr 300
 1096 CCCAGCCTGGGCTTCAGTCCCGTCCAGTTCACCTTCACCTCCAGCTCCACCTATACC 1155
 301 ProGlyAspCysProAsnPheAlaAlaProArgGluValAlaProProTyrGlnGly 320
 1156 CCGGTGTACTGTCCCACTTTCGGGCTCCCGCAGAGAGTGGCACCACTTATCAGGGG 1215
 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
 1216 GCTGACCCCATCTTGCAGACGCTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1275
 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
 1276 TGGGAGGACAGCGCCACAGCCACAGAGCTAGACACTGATGACCCGCGAGCTGTAC 1335
 361 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu 380
 1336 GCGGTGGTGGAGAGCTGCCCTTGGCTGGAGGAATTCGTGCGCGCTTAGGGGTG 1395
 381 SerAspHisGluIleAspArgLeuGluGlnAsnGlyArgCysLeuArgGluAlaGln 400
 1396 AGCGACCAACAGATCGATCGCTGGAGCTGCAGAGCGGCGCTGCTGCGCGAGCGGCA 1455
 401 TyrSerMetLeuAlaThrTrpArgArgThrProArgArgGluAlaThrLeuGluLeu 420
 1456 TACAGCATGCTGGGACCTGGAGCGCGCACCGCGCGCGCGGCGGAGCCAGCTGGAGCTG 1515
 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
 1516 CTGGAGCGGTGCTCCCGCATGGACTGCTGGGCTGCTGGAGGACATGAGGAGGCG 1575
 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
 1576 CTTTGGCGCGCGCGCTCCCGCGCGCGCGCTTCTTCAGA 1620

RESULT 12

ABK13194
 ID ABK13194 standard; DNA; 2161 BP.
 XX
 AC ABK13194;
 DT 23-APR-2002 (first entry)
 XX
 DE Human tumour necrosis factor alpha (TNF alpha) receptor DNA.
 XX
 TNF alpha; apoptosis; ds; tumour; death domain receptor ligand;
 KW diterpenoid triepoxide; cytostatic activity; c-IAP2; c-IAP1;
 KW carcinoma; mammary adenocarcinoma; non-small cell lung carcinoma;
 KW neurological malignancy; haematological malignancy; lichen planus;
 KW non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic;
 KW malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic;
 KW non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour;
 KW T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid;
 KW discoid lupus erythematosus; human; gene; receptor; TNF-R1.
 XX
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 FH 256..1623
 FT CDS
 FT /*tag- a "TNF alpha protein"
 FT /product-
 XX
 PN US6329148-B1.
 XX
 PD 11-DEC-2001.
 XX
 PF 15-FEB-2000; 2000US-0505250.
 XX
 PR 16-FEB-1999; 99US-120313P.
 PR 20-AUG-1999; 99US-149989P.
 XX
 PA (STRD) UNIV LELAND STANFORD.
 XX
 PI Rosen GD, Kao P;
 DR WPI; 2002-121125/16.
 DR P-PSDB; AAU75064.
 XX
 Use of a synergistic combination of death domain receptor ligands and
 diterpenoid triepoxides for killing of tumour cells -
 XX
 Disclosure; Column 23-28; 20pp; English.
 XX
 This invention relates to a novel method for enhanced killing of tumour
 cells comprising contacting a tumour cell with a synergistic
 combination of a death domain receptor ligand and a diterpenoid
 triepoxide. This method has cytostatic activity and works by blocking
 TNF-alpha mediated induction of c-IAP2 and c-IAP1. The method of the
 invention may be used for treating tumours, particularly solid tumours,
 e.g. carcinoma, mammary adenocarcinoma and non-small cell lung carcinoma
 also neurological malignancies, haematological malignancies, e.g.
 cutaneous T-cells, mycosis fungoides, non-MF cutaneous T-cell lymphoma,
 lymphomatoid papulosis, T-cell rich cutaneous lymphoid hyperplasia,
 bullous pemphigoid, discoid lupus erythematosus, lichen planus. The
 combination may be administered with other active agents, e.g. anti-
 metastatic, anti-tumour or anti-angiogenic agents. The potent synergy
 between the diterpenoids and the death domain ligands allows increased
 killing at equivalent or lower doses, and can sensitise otherwise
 resistant cells. This sequence represents the human tumour necrosis
 factor alpha receptor (TNF-R1) DNA. TNF-R1 is a death domain receptor
 used in the used method of the invention in combination with diterpenoid
 triepoxides to kill tumours by inducing apoptosis.
 XX
 SQ Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;
 Alignment Scores:
 Pred. No.: 3.1e-174 Length: 2161

CC Expression of this receptor is regulated by shedding of the
 CC extracellular receptor fragment. The p55 TNF-R can be shed in response
 CC to different inducing agents, e.g. phorbol myristate acetate (PMA),
 CC depending on cell type. The only region of the receptor whose structure
 CC affects the shedding response is the spacer region (see AAR75012) in the
 CC extracellular domain. This region is located close to a site of cleavage
 CC of the molecule, and links the Cys rich module to the transmembrane
 CC domain. The spacer region of the encoded protein was used to create the
 CC chimera between human p55 TNF-R and murine epidermal growth factor
 CC receptor (EGF-R) that are represented by AAR75007-11. This spacer region
 CC was subjected to deletion mutations (AAR75013-25) and substitutions
 CC (AAR75026-47). Of the spacer region, the most important residues are
 CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
 CC important of these. The shedding of the receptor is independent of the
 CC side chain identity of these residues, with the exception of a limited
 CC dependence on the identity of Val 173. Mutations which alter the
 CC conformation of the protein adversely effect the shedding process. The
 CC mutations shown in AAR75013-47 were introduced in order to create an
 CC inhibitor of a protease that is capable of cleaving the soluble TNF-R
 CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in
 CC AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease
 CC inhibitors can be used for enhancing TNF function.

XX Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T; 0 other;

Alignment Scores:

Pred. No.: 3, 12e-174 Length: 2175
 Score: 2487.00 Matches: 455
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 16 Gaps: 0

US-09-899-422a-2 (1-455) x AAQ09513 (1-2175)

QY 1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGluLeuVal 20
 DB 256 ATGGGCTCTCCACGTCGCTGACCTGCTGCTGCGCTGGTGTCTCTCGACCTGTGGTG 315
 QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
 DB 316 GGAATATACCCCTCAGGGGTATTGGACTGCTCCCTCACCTAGGGGACAGGAGAAGA 375
 QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
 DB 376 GATAGTGTGTGTCCTCAAGGAAATATATCCACCTCAAAATAATTTCGATTGTCTGTACC 435
 QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
 DB 436 AAGTCCACAAAGGAACTTACTTGTACAACTGCTCCAGGCCCGGGGACGATACGGAC 495
 QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
 DB 496 TGCAGGAGTGTGAGAGGGCTCTTCCACCGCTTCAGAAACCACCTCAGACACTGCCTC 555
 QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
 DB 556 AGCTGCTCCAATGCCAAAGGAAATGGGTGAGAGATCTCTTCTTCACACAGTGAC 615
 QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
 DB 616 CGGACACCGTGTGGCTGCAGGAAGAACACGATCCCGCATATTGGAGTGAACACCTT 675
 QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
 DB 676 TTCAGTCTCAATTGACGCTCTGCTCAATGGACCGGTGCACCTCTCTCTGCGAGGAG 735
 QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
 DB 736 AAACAGAACACCGTGTGCACCTGCATGTCAGGTTCTTCTTAAGAGAAACAGTGTGTC 795
 QY 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200

DB 796 TCCTCTAGTAAGTAAAGAAAGCCCTGGAGTGCAGAAAGTTGTGCTACCCACAGATTGAG 855
 QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
 DB 856 AATGTTAAGGGCACTGAGGACTCAGGCACACAGTGTGTGGCCCTGGTCAATTCCTTT 915
 QY 221 GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
 DB 916 GGTCTTTGCCCTTTATCCCTCTCTTCAATGTTGTTAAATGATCGCTACCAACGGTGAAG 975
 QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGluGluLeuGlu 260
 DB 976 TCCAAAGCTCTACTCCATCTGTTGTGGAAATCGACACCTGAAAGAGGGGAGCTTAA 1035
 QY 261 GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
 DB 1036 GGAAGTACTACTAAGCCCTTGGCCCAACCAAGCTTCAGTCCACCTCCAGGCTTACC 1095
 QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300
 DB 1096 CCCACCTTGGGCTTTCAGTCCGCTGCCAGTTCCACCTTCAGCTCCAGCTCCACCTATACC 1155
 QY 301 ProGlyAspCysProAsnPheAlaProArgArgGluValAlaProProTyrGlnGly 320
 DB 1156 CCGGTGACTGTCCCACTTTGCGGCTCCCGAGAGAGTGGACACCTATCAGGGG 1215
 QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
 DB 1216 GCTGACCCCATCTTGGCAGAGCTCGCTCGACCCCATCCCAACCCCTTCAGAG 1275
 QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
 DB 1276 TGGAGGAGCAGCGCCACACAGCCACAGACCTAGACACTGATGACCGCGACGCTGTAC 1335
 QY 361 AlaValValGluAsnValProProLeuArgTyrLysGluPheValArgArgLeuGlyLeu 380
 DB 1336 CCGGTGTTGGAGACAGTGCCTCCCTTGGCTGGAAGGAATTCGTGCGGCGCTAGGGCTG 1395
 QY 381 SerAspHisGluIleAspArgLeuLeuGluLeuAsnGlyArgCysLeuArgGluAlaGln 400
 DB 1396 AGCGACACAGAGATCGATCGCTGGAGCTGCAGAACGGCGCTGCTGCGGAGCGCAA 1455
 QY 401 TyrSerMetLeuAlaThrTrpArgArgThrProArgArgGluAlaThrLeuGluLeu 420
 DB 1456 TACAGCATGCTGGGACCTGGAGCGCGCACCGCGCGCGGCGAGCGACGCTGAGCTG 1515
 QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
 DB 1516 CTGGAGCGGTGCTCCGCGACATGGACCTGCTGGCTGCTGGAGGACATCGAGAGCGG 1575
 QY 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
 DB 1576 CTTTGGGCGCGCGCGCTCCCGCGCGCGCGCTCTTCAGAGATCGAGAGCGG 1620
 RESULT 14
 AAQ10955
 ID AAQ10955 standard; cDNA; 2111 BP.
 XX
 AC AAQ10955;
 XX
 DT 24-MAY-1991 (first entry)
 DE Encodes human 55kd TNF-binding protein.
 XX
 KW Tumour Necrosis Factor; binding proteins; septic shock;
 KW autoimmune glomerulonephritis; lymphokine; cytokine.
 FH Key Location/Qualifiers
 FT sig_peptide 187..273 /*tag= a
 FT mat_peptide 274..1551 /*tag= b
 FT /*product= 55kd TNF-BP

DT 13-MAY-1994 (first entry)
 XX p55 Tumour necrosis factor receptor coding sequence.
 DE
 XX
 XX TNF: tumour necrosis factor; receptor; disease; autoimmunity;
 KW rheumatoid arthritis; graft rejection; graft vs. host; septic shock;
 KW effector protein; 88.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 256..1623
 FT /*tag= a
 FT /product= p55 Tumour necrosis factor receptor.
 XX
 XX EP568925-A.
 XX
 XX 10-NOV-1993.
 XX
 XX 29-APR-1993; 93EP-0106981.
 XX
 XX 03-MAY-1992; 92IL-0101769.
 XX
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX
 XX Brakebusch C, Wallach D;
 XX
 XX WPI; 1993-353057/45.
 DR P-PSDB; AAR42197.
 DR
 XX
 XX Modulating activity of tumour necrosis factor receptor - using
 PT peptide(s), antibodies, etc. which interact with critical regions
 PT of receptor or effector protein, for controlling auto-immune
 PT disease, septic shock, etc.
 XX
 XX Claim 2; Figure 1; 17pp; English.
 PS
 XX Modification of the tumour necrosis factor receptor by mutation or
 CC deletion modulates signal transduction and/or cleavage effected by
 CC the receptor. This modulation of activity can also be achieved
 CC using effector proteins which interact with the TNF receptor.
 CC Molecules which interact with the TNF receptor or the effector
 CC proteins can be used to treat or prevent diseases associated with
 CC TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
 CC rejection; graft vs. host disease or septic shock. They can also
 CC be used to treat overdoses of exogenous TNF.
 XX
 XX Sequence 2170 BP; 474 A; 657 C; 584 G; 455 T; 0 other;
 SQ
 Alignment Scores:
 Pred. No.: 1,44e-173 Length: 2170
 Score: 2478.00 Matches: 453
 Percent Similarity: 99.78% Conservative: 1
 Best Local Similarity: 99.56% Mismatches: 1
 Query Match: 99.64% Indels: 0
 DB: 14 Gaps:
 US-09-899-422a-2 (1-455) x AAQ50870 (1-2170)
 Qy 1 MetGlyLeuSerThrValProAspLeuLeuValLeuLeuValLeuVal 20
 Db
 256 ATGGGCTCTCCACCGTGTATGGAGTGTGCTGCTGGCTGGCTGCTGGAGCTTTGGTG 315
 Qy 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGlyLysArg 40
 Db 316 GGAATATACCCCTCAGGGGTTATGGAGTGTGCTGCTCCCTCACCTAGGGGACAGGAGAGA 375
 Qy 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
 Db 376 GATAGTGTGTGCTCCCAAGGAAAAATATCCACCCTCAAAAATAATTCGATTGTGTACC 435
 Qy 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
 Db

Db 436 AAGTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGACGATACGGAC 495
 Qy 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
 Db 496 TGCAGGAGTGTGAGAGCGGCTCTTACCGCTTCAGAAAACCACTCAGACACTGCCTC 555
 Qy 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
 Db 556 AGCTGCTCCAAATGCCAAAGGAATGGTCCAGTGGAGATCTCTTCTTGCACAGTGAC 615
 Qy 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
 Db 616 CGGACACCGTGTGTGGCTGCAGGAAGAACAGTACCGGCTATTATGGAGTGAACCTT 675
 Qy 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
 Db 676 TTCAGTGTTCAAATTCAGAGCTCTGCTCAATGGACCGTGCACCTCTCTCTGCCAGAG 735
 Qy 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
 Db 736 AACAGAACACCGTGTGCACCTGCATGCAGGTTCTTCTTAAGAGAAACAGTGTGTCT 795
 Qy 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
 Db 796 TCCGTGTAGTAACTGTAGAAAAGCCTGCAGTGCAGAGTGTGTGCTTACCCAGATTGAG 855
 Qy 201 AsnValLysGlyThrGluAspSerGlyThrValLeuLeuProLeuValIlePhePhe 220
 Db 856 AATGTTAAGGCACTGAGGACTCAGGCACACAGTGTGTGCTGCTGCTGCTGCTGCTTCT 915
 Qy 221 GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
 Db 916 GGTCTTGGCTTTATCCCTCTCTCTTCAATGTTAATGTATGCTACCAACGGTGGAG 975
 Qy 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeuGlu 260
 Db 976 TCCAGGCTCTACTCCATTGTTGTGGAAATCGACACCTGAANAAGAGGGGAGCTTGA 1035
 Qy 261 GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
 Db 1036 GGAATCTACTAAGCCCTCGCCCAACCAAGCTTCACTCCCACTCCAGGCTTCAAC 1095
 Qy 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300
 Db 1096 CCCACCTTGGGCTTCACTCCCTGCTCCAGTTCACCTTCACTCCAGTCCACGTATACC 1155
 Qy 301 ProGlyAspCysProAsnPheAlaAlaProArgGluValAlaProProTyrGlnGly 320
 Db 1156 CCCGGTGACTGTCCCACTTTCGGCTCCCGCAGAGAGGTGGCACCACTATCAGGGG 1215
 Qy 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
 Db 1216 GCTGACCCCATCTTGGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAAGAG 1275
 Qy 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
 Db 1276 TGGAGGACACGCCCAAGCCACAGCCCTAGACACTGATGATCCCGCGCAGCTGTAC 1335
 Qy 361 AlaValValGluAsnValProProLeuArgTyrLysGluPheValArgLeuGlyLeu 380
 Db 1336 GCCGTGGTGAGAACAGTGGCCCCCTTGGCTGGGAAGGAATTCGTGGCGCGCTAGGGCTG 1395
 Qy 381 SerAspHisGluIleAspArgLeuGluLeuAsnGlyArgCysLeuArgGluAlaGln 400
 Db 1396 AGCCACACAGAGATCGATCGGCTGAGCTGCAGAACGGCGCTGCTGCGGAGGCGCAA 1455
 Qy 401 TyrSerMetLeuAlaThrTrpArgArgThrProArgArgGluAlaThrLeuGluLeu 420
 Db 1456 TACAGCATGCTGGCGACCTGGAGGCGGCACCGCGCGGAGGAGGAGGAGGAGGAG 1515
 Qy 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
 Db 1516 CTGGAGCGGCTCCCGGACATGCACCTGCTGGGCTGCTGGAGGAGATCGAGAGGCGG 1575

QY 441 LeuCysGlyProAlaLeuProAlaProSerLeuLeuArg 455
Db 1576 CTTTCGGCGCGCGCGCTCCCGCCGCCAGCTTCTCAGA 1620

Search completed: June 9, 2003, 01:23:24
Job time : 322 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 20:42:48 ; Search time 344 Seconds
(without alignments)
8955.621 Million cell updates/sec

Title: US-09-899-422A-1

Perfect score: 1368

Sequence: 1 atgggccttcacccgtgcc.....cggccagcttcttcagatga 1368

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1366.4	99.9	1368	14	AAQ49932
2	1366.4	99.9	1368	14	AAQ95105
3	1366.4	99.9	2088	12	AAQ10883
4	1366.4	99.9	2088	22	AAQ83946
5	1366.4	99.9	2111	20	AAQ09170
6	1366.4	99.9	2111	22	AAQ48859
7	1366.4	99.9	2111	24	ABK84039
8	1366.4	99.9	2111	24	ABN95862
9	1366.4	99.9	2161	21	AAZ48475

10	1366.4	99.9	2161	24	ABK13194	Human tumour necro
11	1364.8	99.8	2111	12	AAQ10955	Encodes human 55kD
12	1364.8	99.8	2175	16	AAQ90513	p55 TNF-R gene. H
13	1363.2	99.6	2062	13	AAQ20973	TNF-alpha binding
14	1363.2	99.6	2062	13	AAQ24440	Encodes TNF-alpha
15	1363.2	99.6	2176	12	AAQ12215	Type I TNF receptor
16	1361.6	99.4	2141	11	AAQ06285	Human Tumour Necro
17	1360	99.4	2170	14	AAQ05870	p55 Tumour necrosi
18	1120.4	81.9	1334	11	AAQ06282	Plasmid Tumour Nec
19	743.4	54.3	2130	24	ABK63694	Rat sequence diffe
20	732.2	53.5	2173	11	AAQ06284	Rat Tumour Necrosi
21	632.8	46.3	6926	18	AAV04431	Vector pcDNA3-1961
22	632.4	46.2	6889	17	AAV15931	DHFR/Intron (Wtras
23	596.8	43.6	608	13	AAQ24441	Encodes truncated
24	515.4	37.7	1478	20	AAQ58150	CadC-fusion polyype
25	514	37.6	1301	18	AAQ94022	CDNA for TBP(20-19
26	506	37.0	1147	18	AAQ94021	CDNA for TBP(20-19
27	501.4	36.7	504	13	AAQ24445	Encodes truncated
28	483	35.3	483	19	AAV41548	Human soluble tumo
29	483	35.3	483	19	AAV19801	Soluble tumour nec
30	483	35.3	483	20	AAV81732	Tumour necrosis in
31	483	35.3	483	22	AAQ83945	Human 30 kDa TNF i
32	440	32.2	2254	21	AAQ95104	Partial human TNFR
33	424.4	31.0	1049	18	AAQ94007	CDNA for TBP(20-16
34	424.4	31.0	1202	18	AAQ94008	CDNA for TBP(20-16
35	418	30.6	1674	21	AAZ50196	Male fusion plasmid
36	381	27.9	1977	24	ABA99913	TNF-selectokine pr
37	376.2	27.5	477	13	AAQ24444	Encodes truncated
38	375.8	27.5	507	24	ABL99490	Target canine gene
39	357.2	26.1	474	13	AAQ24442	Encodes truncated
40	329.6	22.1	5870	21	AAV15044	Nucleotide sequenc
41	312.4	22.8	339	19	AAV19804	Truncated stNFR, s
42	310.8	22.7	462	13	AAQ24443	Encodes truncated
43	308.2	22.5	333	19	AAV19805	Truncated stNFR, s
44	304.4	22.3	332	19	AAV19803	Truncated stNFR, s
45	294.6	21.5	315	19	AAV19806	Truncated stNFR, s

ALIGNMENTS

RESULT 1

AAQ49932
ID AAQ49932 standard; cDNA to mRNA; 1368 BP.

XX AAQ49932;

XX 29-APR-1994 (first entry)

XX Lambda-derived TNF-R cDNA.

XX Human; tumour necrosis factor receptor; TNF-R; Interleukin-1 receptor;
KW IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW graft versus host disease; sepsis; inflammation; allergy;
KW autoimmune dysfunction; ss.
XX Homo sapiens.
OS Lambda-gt10-7-ctnfbp.

Key	Location/Qualifiers
FT CDS	1..1366
FT	/*tag= a
FT	/product= hTNF-R
FT	1..120
FT	/*tag= b
FT	mat_peptide
FT	121..1363
FT	/*tag= c
PN	WO9319777-A.
PD	14-OCT-1993.

Db 427 TGCAGGAGTGTGACGCGGCTCTTTCACCGCTTCAGAAACACCTCAGACACTGCCTC 486
QY 301 AGTGTCTCCAAATGCCAAAGAAATGGGTGAGTGTGAGATCTCTTTCACACAGTGAC 360
Db 487 AGTGTCTCCAAATGCCAAAGAAATGGGTGAGTGTGAGATCTCTTTCACACAGTGAC 546
QY 361 CGGACACCGTGTGGTGTGAGGAGACACAGTACCGGCAATTAATGAGTGAACACCTT 420
Db 547 CGGACACCGTGTGGTGTGAGGAGACACAGTACCGGCAATTAATGAGTGAACACCTT 606
QY 421 TTCAGTGTCTCAATGTCAGCTCTGCTCAATGGACCGTGCACCTCTCTCTGCCAGAG 480
Db 607 TTCAGTGTCTCAATGTCAGCTCTGCTCAATGGACCGTGCACCTCTCTCTGCCAGAG 666
QY 481 AACAGAACACCGTGTGCACCTGCCATGCAGTGTCTTCTTAAGAGAAACAGTGTGTC 540
Db 667 AACAGAACACCGTGTGCACCTGCCATGCAGTGTCTTCTTAAGAGAAACAGTGTGTC 726
QY 541 TCCTGTAGTAACTGTAGAAAGCTGTGAGTGCAGGAAGTGTGCTACCCAGATTGAG 600
Db 727 TCCTGTAGTAACTGTAGAAAGCTGTGAGTGCAGGAAGTGTGCTACCCAGATTGAG 786
QY 601 AATGTTAAGGCACTGAGGACTCAGGCACACAGTGTGTTGCCCTGCTCATTTCTTT 660
Db 787 AATGTTAAGGCACTGAGGACTCAGGCACACAGTGTGTTGCCCTGCTCATTTCTTT 846
QY 661 GGTCTTTGCCCTTTATCCCTCTCTTCAATGCTTTAATGTATCGCTACCAACGGTGAAG 720
Db 847 GGTCTTTGCCCTTTATCCCTCTCTTCAATGCTTTAATGTATCGCTACCAACGGTGAAG 906
QY 721 TCCAGGCTCTACTCAATGTTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGA 780
Db 907 TCCAGGCTCTACTCAATGTTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGA 966
QY 781 GGAATCTACTAAGCCCTTGGCCCAACCAAGCTTCAGTCCACCTCCAGGCTTACC 840
Db 967 GGAATCTACTAAGCCCTTGGCCCAACCAAGCTTCAGTCCACCTCCAGGCTTACC 1026
QY 841 CCCACCTGGGCTTCACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 900
Db 1027 CCCACCTGGGCTTCACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1086
QY 901 CCCGCTGCTCTCCCACTTTCGCGCTCCCGCAGAGAGTGGCACCACCTATCAGGG 960
Db 1087 CCCGCTGCTCTCCCACTTTCGCGCTCCCGCAGAGAGTGGCACCACCTATCAGGG 1146
QY 961 GCTGACCCCATCTTGGACAGCCCTCGCTCCGACCCCACTCCCAACCCCTTCAGAG 1020
Db 1147 GCTGACCCCATCTTGGACAGCCCTCGCTCCGACCCCACTCCCAACCCCTTCAGAG 1206
QY 1021 TGGGAGGACAGCCGACCAAGCCACAGACCTAGACACTGATGACCCGCGACGCTGAC 1080
Db 1207 TGGGAGGACAGCCGACCAAGCCACAGACCTAGACACTGATGACCCGCGACGCTGAC 1266
QY 1081 GCCGTGTGGAGAGCTGCCCCGCTGCTGCTGGAAGGAAATTCGTGCGCGCTTAGGCTG 1140
Db 1267 GCCGTGTGGAGAGCTGCCCCGCTGCTGCTGGAAGGAAATTCGTGCGCGCTTAGGCTG 1326
QY 1141 AGCCACACAGAGATCGATCGGCTGGAGCTGCAGAACCGGCGCTGCTGCGGAGCGCAA 1200
Db 1327 AGCCACACAGAGATCGATCGGCTGGAGCTGCAGAACCGGCGCTGCTGCGGAGCGCAA 1386
QY 1201 TACAGCATGCTGGGACCTGAGGCGGCGACCGCGCGGCGGCGGCGGCGGCGGCGGCTG 1260
Db 1387 TACAGCATGCTGGGACCTGAGGCGGCGACCGCGCGGCGGCGGCGGCGGCGGCGGCTG 1446
QY 1261 CTGGGCGCGCTGCTGCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
Db 1447 CTGGGCGCGCTGCTGCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1506
QY 1321 CTTTTCGCGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
Db 1507 CTTTTCGCGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1554

RESULT 7
ABK84039

ID ABR84039 standard; cDNA; 2111 BP.

XX ABR84039;

XX 14-AUG-2002 (first entry)

XX Human cDNA differentially expressed in granulocytic cells #610.

Human; ss; granulocytic cell; DNA chip; bacterial infection;
viral infection; parasitic infection; protozoal infection;
fungal infection; sterile inflammatory disease; psoriasis;
rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
cardiac reperfusion injury; renal reperfusion injury; ARDS;
adult respiratory distress syndrome; inflammatory bowel disease;
Crohn's disease; ulcerative colitis; periodontal disease;
granulocyte activation; chronic inflammation; allergy.

OS Homo sapiens.

XX WO200228999-A2.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US30821.

XX 03-OCT-2000; 2000US-237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX WPI; 2002-435328/46.

Detecting granulocyte activation by detecting differential expression
of genes associated with granulocyte activation, which serves as
diagnostic markers that is useful for monitoring disease states and
drug toxicity

Claim 1; SEQ ID No 610; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation
(GCA), by detecting the level of expression of gene(s) (Gs) identified by
DNA chip analysis as given in the specification, and comparing
the expression level to an expression level in an unactivated
GC, where differential expression of Gs is indicative of GCA.

Also included are modulating (M2) GA by contacting GC with an agent
that alters the expression of at least one gene in Gs; (2) screening (M3)
for an agent capable of modulating GCA or an inflammation (especially
chronic) in a tissue, an allergic response in a subject, exposure of a
subject to a pathogen or sterile inflammatory disease using the
gene expression profile; (3) detecting (M4) an inflammation (especially
chronic) in a tissue, an allergic response in a subject, exposure of a
subject to a pathogen or sterile inflammatory disease, by detecting the
level of expression in a sample of the tissue of gene(s) from Gs, where
the level of expression of the gene is indicative of inflammation;

(4) treating (M5) an inflammation (especially chronic) or in a tissue,
an allergic response in a subject, exposure of a subject to a pathogen
or sterile inflammatory disease, by contacting a tissue having
inflammation with an agent that modulates the expression of gene(s)
from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
modulating GA; M3 is useful for screening an agent capable of modulating
detecting an inflammation (especially chronic) in a tissue, an allergic
response in a subject, exposure of a subject to a pathogen or sterile
inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
reperfusion injury, ARDS, adult respiratory distress syndrome,
inflammatory bowel disease, Crohn's disease, ulcerative colitis,
periodontal disease; also bacterial infection, viral infection,

CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2111 BP; 445 A; 629 C; 587 G; 450 T; 0 other;
Query Match 99.9%; Score 1366.4; DB 24; Length 2111;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGGCGCTTCCACCGTGCCTGACCTGCTGCTGCACCTGGTCTCCTCGAGCTGTGGTG 60
DB 187 ATGGGCGCTTCCACCGTGCCTGACCTGCTGCTGCCTGGTCTCCTCGAGCTGTGGTG 246
QY 61 GGAATATACCCCTCAGGGGTTATTCGACTGTGTCCTACCTAGGGGACAGGAGAGAGA 120
DB 247 GGAATATACCCCTCAGGGGTTATTCGACTGTGTCCTACCTAGGGGACAGGAGAGAGA 306
QY 121 GATAGTGTGTGCCCAAGGAAATATATCCACCTCAAAATAATTCGATTTCGTGTACC 180
DB 307 GATAGTGTGTGCCCAAGGAAATATATCCACCTCAAAATAATTCGATTTCGTGTACC 366
QY 181 AAGTCCCAAGAACCTACTGTACATGACTTCCAGGCGCGGGGACGATACGGAC 240
DB 367 AAGTCCCAAGAACCTACTGTACATGACTTCCAGGCGCGGGGACGATACGGAC 426
QY 241 TCCAGGGAGTGTACAGCGGCTCTTCCACCGTTCAGAAACACCTCAGACACTGCCTC 300
DB 427 TCCAGGGAGTGTACAGCGGCTCTTCCACCGTTCAGAAACACCTCAGACACTGCCTC 486
QY 301 AGCTGCTCCAAATGCCGAAAGGAAATGGTCAAGTGGAGATCTCTTTTGCACATGGAC 360
DB 487 AGCTGCTCCAAATGCCGAAAGGAAATGGTCAAGTGGAGATCTCTTTTGCACATGGAC 546
QY 361 CGGGACACCGTGTGGCTGCAGGAAGAACCAAGTACCGGCATTTATGGAGTGAACACCTT 420
DB 547 CGGGACACCGTGTGGCTGCAGGAAGAACCAAGTACCGGCATTTATGGAGTGAACACCTT 606
QY 421 TTCCAGTGTCAATTTGACGCTCTGCTCAATGGACCGTGCACCTCTCCTGCCAGAG 480
DB 607 TTCCAGTGTCAATTTGACGCTCTGCTCAATGGACCGTGCACCTCTCCTGCCAGAG 666
QY 481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTTAAAGAGAAAGAGTGTCTC 540
DB 667 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTTTAAAGAGAAAGAGTGTCTC 726
QY 541 TCCTGTAGTACTGTAAAGAACCGTGCAGTGCAGGAGTGTGCTTACCCAGATTGAG 600
DB 727 TCCTGTAGTACTGTAAAGAACCGTGCAGTGCAGGAGTGTGCTTACCCAGATTGAG 786
QY 601 AATGTTAAGGACCTGAGGACTCAGGCACACAGTGTGTCCTGCTGCTCATTTTCTTTT 660
DB 787 AATGTTAAGGACCTGAGGACTCAGGCACACAGTGTGTCCTGCTGCTCATTTTCTTTT 846
QY 661 GGTCTTTCCCTTTTATCCCTCTCTTCATTTGTTTAAATGTATGCTTACCAACGGTGAAG 720
DB 847 GGTCTTTCCCTTTTATCCCTCTCTTCATTTGTTTAAATGTATGCTTACCAACGGTGAAG 906
QY 721 TCCAGGCTTACTGATTTGTTGGGAAATCGACACCTGAAAGAGGGGGAGCTTGA 780
DB 907 TCCAGGCTTACTGATTTGTTGGGAAATCGACACCTGAAAGAGGGGGAGCTTGA 966
QY 781 GGAAGTACTACTAGGCGCTTGGCCCCCAACCCAGCTTCAGTCCCACTCCAGGCTTACC 840

DB 967 GGAAGTACTACTAGGCGCTTGGCCCCCAACCCAGCTTCAGTCCCACTCCAGGCTTACC 1026
QY 841 CCCACCCCTGGGCTTCAGTCCCGTGCAGTCCCACTTCACCTCCAGCTTCACCTTATACC 900
DB 1027 CCCACCCCTGGGCTTCAGTCCCGTGCAGTCCCACTTCACCTTCAGCTCCAGCTTATACC 1086
QY 901 CCCGCTGACTGTGCCCAACTTTTGGCGCTCCCCGACAGAGGTGGCACCACTTATCAGGG 960
DB 1087 CCCGCTGACTGTGCCCAACTTTTGGCGCTCCCCGACAGAGGTGGCACCACTTATCAGGG 1146
QY 961 GCTGACCCCATCTTTCGACAGCCCTCCGCTCCGACCCCATCCCAACCCCTTTCAGAG 1020
DB 1147 GCTGACCCCATCTTTCGACAGCCCTCCGCTCCGACCCCATCCCAACCCCTTTCAGAG 1206
QY 1021 TGGGAGGACAGCGCCCAACAGCCACAGAGCTTAGACACTGATGACCCGCGACGCTGTAC 1080
DB 1207 TGGGAGGACAGCGCCCAACAGCCACAGAGCTTAGACACTGATGACCCGCGACGCTGTAC 1266
QY 1081 GCCGTGTGGAGAACCTGCCCGCTTGGCTGGAAAGAAATTCGTGCGGCGCTTAGGGCTG 1140
DB 1267 GCCGTGTGGAGAACCTGCCCGCTTGGCTGGAAAGAAATTCGTGCGGCGCTTAGGGCTG 1326
QY 1141 AGCGACACAGAGATCGATCGGCTGAGCTGCAGAACGGCGCTGCTGCGGAGGCGCAA 1200
DB 1327 AGCGACACAGAGATCGATCGGCTGAGCTGCAGAACGGCGCTGCTGCGGAGGCGCAA 1386
QY 1201 TACAGCATGTGGGACCTGGAGGCGCGCACCGCGCGGAGGCGGAGGCGGAGGCTG 1260
DB 1387 TACAGCATGTGGGACCTGGAGGCGCGCACCGCGCGGAGGCGGAGGCGGAGGCTG 1446
QY 1261 CTGGGACCGTGTCTCCGACATGACCTGCTGGCTGGCTGGAGGACATCGAGAGGCG 1320
DB 1447 CTGGGACCGTGTCTCCGACATGACCTGCTGGCTGGCTGGAGGACATCGAGAGGCG 1506
QY 1321 CTTTTCGCGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
DB 1507 CTTTTCGCGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1554
RESULT 9
AAZ48475
ID AAZ48475 standard; DNA; 2161 BP.
XX
AC AAZ48475;
XX
DT 31-MAR-2000 (first entry)
XX
DE Human tumour necrosis factor receptor (TNFR1) nucleotide sequence.
XX
KW Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
XX inflammation; tumour formation; TNFR1; anticancer; ds.
OS Homo sapiens.
XX
PN US6007995-A.
XX
PD 28-DEC-1999.
XX
PF 26-JUN-1998; 98US-0106038.
XX
PR 26-JUN-1998; 98US-0106038.
XX
PA (ISIS-) ISIS PHARM. INC.
XX Baker BF, Cowser LM;
XX
DR WPI; 2000-105333/09.
XX
PT Antisense inhibition of tumor necrosis factor type 1 expression for
XX diagnosis, treatment and prevention of disease, particularly tumors
PS Example 10; Columns 33-36; 34pp; English.

AC AAQ90513;
 XX 19-JAN-1996 (first entry)
 XX p55 TNF-R gene.
 XX p55; tumour necrosis factor receptor; TNF-R; human; murine; chimera;
 KW epidermal growth factor receptor; EGF-R; protease; inhibitor;
 KW phorbol myristate acetate; PMA; ss.
 XX Homo sapiens.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 256..1623
 FT /*tag= a
 FT /product= p55 TNF-R
 FT 2143..2149
 FT misc_signal
 FT /*tag= b
 FT /note= "possible poly-A signal"
 XX
 XX AU9475742-A.
 PN
 XX
 XX 04-MAY-1995.
 PD
 XX
 XX 11-OCT-1994; 94AU-0075742.
 PF
 XX
 XX 12-OCT-1993; 93IL-0107268.
 PR
 XX
 XX (YEDA) YEDA RES & DEV CO LTD.
 PA
 XX
 XX Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
 PI
 XX
 XX WPI; 1995-194342/26.
 DR P-PSDB; AAR75084.
 XX
 XX New protease capable of cleaving soluble tumour necrosis factor
 PT (TNF) receptor - from cell-bound TNF- receptor, useful for
 PT antagonising deleterious effects of TNF.
 XX
 XX Disclosure; Fig 1; 40pp; English.
 PS
 XX This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.
 CC Expression of this receptor is regulated by shedding of the
 CC extracellular receptor fragment. The p55 TNF-R can be shed in response
 CC to different inducing agents, e.g. phorbol myristate acetate (PMA),
 CC depending on cell type. The only region of the receptor whose structure
 CC affects the shedding response is the spacer region (see AAR75012) in the
 CC extracellular domain. This region is located close to a site of cleavage
 CC of the molecule, and links the Cys rich module to the transmembrane
 CC domain. The spacer region of the encoded protein was used to create the
 CC chimeras between human p55 TNF-R and murine epidermal growth factor
 CC receptor (EGF-R) that are represented by AAR75007-11. This spacer region
 CC was subjected to deletion mutations (AAR75013-25) and substitutions
 CC (AAR75026-47). Of the spacer region, the most important residues are
 CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
 CC important of these. The shedding of the receptor is independent of the
 CC side chain identity of these residues, with the exception of a limited
 CC dependence on the identity of val 173. Mutations which alter the
 CC conformation of the protein adversely effect the shedding process. The
 CC mutations shown in AAR75013-47 were introduced in order to create an
 CC inhibitor of a protease that is capable of cleaving the soluble TNF-R
 CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in
 CC AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease
 CC inhibitors can be used for enhancing TNF function.
 XX
 XX Sequence 2175 BP; 474 A; 642 C; 603 G; 456 T; 0 other;
 SQ
 Query Match 99.8%; Score 1364.8; DB 16; Length 2175;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGGGCCCTCTCACCGTGCCTGACTGCTGCTGCACCTGGTCTCTCTGAGAGCTGTGGTG 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 256 ATGGCCCTCTCCACCGTGCCTGACCTGCTGCTGCGGTGGTGTCTCTTGGAGAGCTGTGGTG 315
 QY 61 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGACAGGAGAGAGA 120
 Db 316 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGACAGGAGAGAGA 375
 QY 121 GATAGTGTGTGCCCAAGSAAATATATCCACCTCAAAATAATTCGATTGTGTACC 180
 Db 376 GATAGTGTGTGCCCAAGSAAATATATCCACCTCAAAATAATTCGATTGTGTACC 435
 QY 181 AAGTCCCAAAAGGACCTACTTGTACAAATGACTGTCCAGGCCCGGGCAGATACGAC 240
 Db 436 AAGTCCCAAAAGGACCTACTTGTACAAATGACTGTCCAGGCCCGGGCAGATACGAC 495
 QY 241 TGCAGGGAGTGTGAGAGCGCTCTTACCGCTTCAGAAAACACCTCAGACACTGCCTC 300
 Db 496 TGCAGGGAGTGTGAGAGCGCTCTTACCGCTTCAGAAAACACCTCAGACACTGCCTC 555
 QY 301 AGCTGCTCCAAATGCCAAAGGAATAGGTGAGTGGAGATCTCTTCTTGACAGTGGAC 360
 Db 556 AGCTGCTCCAAATGCCAAAGGAATAGGTGAGTGGAGATCTCTTCTTGACAGTGGAC 615
 QY 361 CGGGACACCGTGTGGCTGCAGGAAGAACAGTACCGGCATTTATTTGAGTGAACCTT 420
 Db 616 CGGGACACCGTGTGGCTGCAGGAAGAACAGTACCGGCATTTATTTGAGTGAACCTT 675
 QY 421 TTCAGTGTCTCAATTCAGCGCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGAG 480
 Db 676 TTCAGTGTCTCAATTCAGCGCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGAG 735
 QY 481 AACAGAACACCGTGTGCACCTGCCATGCGAGGTTTCTTCTTAAGAGAAAACAGTGTGTC 540
 Db 736 AACAGAACACCGTGTGCACCTGCCATGCGAGGTTTCTTCTTAAGAGAAAACAGTGTGTC 795
 QY 541 TCCTGTAGTAACTGTAAGAAAAGCTGGAGTGCAGAGTTGTGCTCCTCCACCCAGATTGAG 600
 Db 796 TCCTGTAGTAACTGTAAGAAAAGCTGGAGTGCAGAGTTGTGCTCCTCCACCCAGATTGAG 855
 QY 601 AATGTTAAGGCACTGAGGACTCAGGCACACAGTGTGTTGCCCTCGTCTATTTCTTT 660
 Db 856 AATGTTAAGGCACTGAGGACTCAGGCACACAGTGTGTTGCCCTCGTCTATTTCTTT 915
 QY 661 GGTCTTTGCCCTTTATCCCTCTCTTCAATGGTTTATGTATCGTACCACAGTGGAG 720
 Db 916 GGTCTTTGCCCTTTATCCCTCTCTTCAATGGTTTATGTATCGTACCACAGTGGAG 975
 QY 721 TCCAAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAAGAGGGGAGCTTGA 780
 Db 976 TCCAAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAAGAGGGGAGCTTGA 1035
 QY 781 GGAATCTACTAAGCCCTCGCCCAAAACCCAGCTTCAGTCCACCTCCAGGCTTACC 840
 Db 1036 GGAATCTACTAAGCCCTCGCCCAAAACCCAGCTTCAGTCCACCTCCAGGCTTACC 1095
 QY 841 CCCACCTCGGGCTTCAGTCCCGTCCAGTTCACCTTCCCTCCAGCTCCACCTATACC 900
 Db 1096 CCCACCTCGGGCTTCAGTCCCGTCCAGTTCACCTTCCCTCCAGCTCCACCTATACC 1155
 QY 901 CCCGCTGACTCTCCCACTTTTCGGGCTCCCGCAGAGAGTGGACACCACTATCAGGGG 960
 Db 1156 CCCGCTGACTCTCCCACTTTTCGGGCTCCCGCAGAGAGTGGACACCACTATCAGGGG 1215
 QY 961 GCTGACCCCACTCTCTGGGACAGCCCTCGCCTCCGACCCCACTCCCAAGCCCTTCAGAG 1020
 Db 1216 GCTGACCCCACTCTCTGGGACAGCCCTCGCCTCCGACCCCACTCCCAAGCCCTTCAGAG 1275
 QY 1021 TGGGAGGACAGGCCCAACAGCCACAGAGCTTAGACACTGATGACCCCGCAGCTGTAC 1080
 Db 1276 TGGGAGGACAGGCCCAACAGCCACAGAGCTTAGACACTGATGACCCCGCAGCTGTAC 1335
 QY 1081 CCCCTGTGTGAGAGAGCTGCCCGCTTGGCTGTGGAAGAAATTCGTGCGGCGCTTAGGGCTG 1140
 Db 1336 CCCCTGTGTGAGAGAGCTGCCCGCTTGGCTGTGGAAGAAATTCGTGCGGCGCTTAGGGCTG 1395


```
QY 961 GCTGACCCCATCTTGGGACAGCCCTCGCCTCCGACCCCATCCCAACCCCTTCAGAAG 1020
DB 1115 GCTGACCCCATCTTGGGACAGCCCTCGCCTCCGACCCCATCCCAACCCCTTCAGAAG 1174
QY 1021 TGGGAGGACAGCCGACAGCCACAGAGCCCTAGACACTGATACCCGCGACGCTGTAC 1080
DB 1175 TGGGAGGACAGCCGACAGCCACAGAGCCCTAGACACTGATACCCGCGACGCTGTAC 1234
QY 1081 GCCGTGGTGGAGACGTCGCCCGCTTGGGCTGGAAGGAATTCGTGGCGGCCCTAGGGCTG 1140
DB 1235 GCCGTGGTGGAGACGTCGCCCGCTTGGGCTGGAAGGAATTCGTGGCGGCCCTAGGGCTG 1294
QY 1141 ACCGACACAGAGATCGATCGGCTGAGCTGCAGACGGCGCTGCTCGCGAGCGCAA 1200
DB 1295 ACCGACACAGAGATCGATCGGCTGAGCTGCAGACGGCGCTGCTCGCGAGCGCAA 1354
QY 1201 TACACATCTGCTGGACACTGGAGCGGCGACGCGCGCGGCGGAGCCACGCTGAGCTG 1260
DB 1355 TACACATCTGCTGGACACTGGAGCGGCGACGCGCGGCGGAGCCACGCTGAGCTG 1414
QY 1261 CTGGACGCGTCTCCGCGACATGACCTGCTGGGCTGCCCTGGAGGACATCGAGGCGC 1320
DB 1415 CTGGACGCGTCTCCGCGACATGACCTGCTGGGCTGCCCTGGAGGACATCGAGGCGC 1474
QY 1321 CTTTGGGCGCGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
DB 1475 CTTTGGGCGCGCGCGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1522
```

RESULT 14

AAQ24440

ID AAQ24440 standard; DNA; 2062 BP.

XX AC AAQ24440;

XX 05-NOV-1992 (first entry)

DE Encodes TNF-alpha 55KD receptor.

XX tumour necrosis factor alpha; extracellular binding domain;
KW treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW malaria; viral meningitis; graft versus host disease;
KW autoimmune disease; rheumatoid arthritis.

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 156..1517
FT /tag= a
FT /product= human TNF-alpha
FT 1265..1267
FT /tag= b
FT /note= "3"
FT 1265..1267
FT /tag= c
FT /codon= seq: "TGG", aa: Thr
FT 1258..1260
FT /tag= d
FT /codon= Seq "AAG", aa: Leu
FT 1433..1435
FT /tag= e
FT /codon= Seq: "GAC", aa: Asn
FT 156..274
FT /tag= f

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

FT mat_peptide

XX

PA

XX

PI

XX

DR

DR

XX

PT

PT

PT

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

XX

SQ

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

(CHAR-) CHARING CROSS SUNLEY RES CENT.
Brennan EM, Feldmann M, Gray PW, Turner MJC;
WPI: 1992-167156/20.
P-PSDB; AAR24000.

New polypeptide capable of binding human TNF alpha - comprises
first three cysteine-rich subdomains of TNF alpha receptor for
treating autoimmune disease, septic shock, HIV etc.

Claim 4; Fig 1; 43pp; English.

This sequence encodes human TNF-alpha 55KD receptor. A placenta cDNA
library in gt10 was screened with probe AAQ29236. Ten hybridising clones
were plaque purified and cDNA size determined by PAGE against an
Eco RI digested phage DNA. The inserts of two cDNA clones were then
sequenced. The coding region of the majority of the human TNF-alpha
55KD receptor was isolated as an EcoRI fragment encoding 374 amino
acids, and cloned into a mammalian cell expression vector, resulting
in pTNFR. A derivative of the TNF-alpha receptor was produced by
engineering a termination codon just prior to the transmembrane
domain. PCR with primers AAQ29237,8 generated a 300bp
restriction fragment which was cloned into pTNFR, giving pTNFRcd.
DNA sequencing confirmed this contained the designed DNA sequence.
The TNF-alpha receptor expression plasmids were then transfected
into monkey COS-7 cells.

See also AAQ24440-51, AAR24000, AAR24080-84, AAR27585, AAQ29236-8

Sequence 2062 BP; 429 A; 618 C; 572 G; 443 T; 0 other;

Query Match 99.6%; Score 1363.2; DB 13; Length 2062;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1365; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 ATGGCCCTCTCCACCGTGCCTGACCTGCTGCTGCACCTGGTGTCTCTGAGCTGTGGTG 60

155 ATGGCCCTCTCCACCGTGCCTGACCTGCTGCTGCACCTGGTGTCTCTGAGCTGTGGTG 214

61 GGAATATACCCCTCAGGGGTATTGGAGTGTGCTCCTACCTAGGGGACAGGAGAGA 120

215 GGAATATACCCCTCAGGGGTATTGGAGTGTGCTCCTACCTAGGGGACAGGAGAGA 274

121 GATAGTGTGTGCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGTGTACC 180

275 GATAGTGTGTGCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGTGTACC 334

181 AAGTCCACAAAGGAACTACTTGTACATGCTGCTCCAGCCCGGGGACGATACGAC 240

335 AAGTCCACAAAGGAACTACTTGTACATGCTGCTCCAGCCCGGGGACGATACGAC 394

241 TGCAGGGAGTGTGAGAGCGGCTCCTTACCGCTTCAGAAAACCCACCTCAGACACGCTC 300

395 TGCAGGGAGTGTGAGAGCGGCTCCTTACCGCTTCAGAAAACCCACCTCAGACACGCTC 454

301 AGCTGCTCCAAATGCCAAAGGAAATGGGTGAGTGTGAGTGTGCTTCTTTCACAGTGCAC 360

455 AGCTGCTCCAAATGCCAAAGGAAATGGGTGAGTGTGAGTGTGCTTCTTTCACAGTGCAC 514

361 CGGACACCGTGTGCTGCTGAGGAGAACACAGTACCGGCAATATTGGAGTGAACCTT 420

515 CGGACACCGTGTGCTGCTGAGGAGAACACAGTACCGGCAATATTGGAGTGAACCTT 574

421 TTCCAGTGTTCATTTGAGGCTGCTGCTCAATGGGCGGCTGCTCCTCTCTCCAGGAG 480

575 TTCCAGTGTTCATTTGAGGCTGCTGCTCAATGGGCGGCTGCTCCTCTCTCCAGGAG 634

481 AAACAGAACACCGTGTGCTGCTGAGGAGAACACAGTACCGGCAATATTGGAGTGAACCTT 540

635 AAACAGAACACCGTGTGCTGCTGAGGAGAACACAGTACCGGCAATATTGGAGTGAACCTT 694

541 TCCTGTAGTAACTGTGAAGAAAGCTGGAGTGCAGGAGTGTGCTTACCCACGATTTAG 600

```
Db 695 TCCTGTAGTAACGTAAAGAAAGCCCTGGAGTGCAGAGTTGTGCTACCCAGATGTAG 754
QY 601 AATGTTAAGGCACTGAGCACTCAGCACCAGCACTGCTGTCCTCCCTGCTCATTTCTTT 660
Db 755 AATGTTAAGGCACTGAGCACTCAGCACCAGCACTGCTGTCCTCCCTGCTCATTTCTTT 814
QY 661 GGTCTTTGCTTTTATCCCTCTCTCTCATTTGTTTAAATGATATCGTACCAACGGTGGAG 720
Db 815 GGTCTTTGCTTTTATCCCTCTCTCTCATTTGTTTAAATGATATCGTACCAACGGTGGAG 874
QY 721 TCAAGCTCTACTCCATCTTTTGTGGAAATCGACACCTGAAAGAGGGGAGCTTGA 780
Db 875 TCAAGCTCTACTCCATCTTTTGTGGAAATCGACACCTGAAAGAGGGGAGCTTGA 934
QY 781 GGAACCTACTAAGCCCTGCCCCAAACCAAGCTTCAGTCCCACTCCAGCTTCACC 840
Db 935 GGAACCTACTAAGCCCTGCCCCAAACCAAGCTTCAGTCCCACTCCAGCTTCACC 994
QY 841 CCCACCTGGCTTCACTCCCTGCCCCAGTTCACCTTCACCTCCAGCTTCACCTATACC 900
Db 995 CCCACCTGGCTTCACTCCCTGCCCCAGTTCACCTTCACCTTCACCTTCACCTATACC 1054
QY 901 CCGGTGACTGCCCAACTTTGCGCTCCCGCAGAGGTGGCACCACCTATCAGGG 960
Db 1055 CCGGTGACTGCCCAACTTTGCGCTCCCGCAGAGGTGGCACCACCTATCAGGG 1114
QY 961 GGTGACCCCATCTTGGCAGACCCCTGCGCTCCGACCCCATCCCAACCCCTTCAGAA 1020
Db 1115 GGTGACCCCATCTTGGCAGACCCCTGCGCTCCGACCCCATCCCAACCCCTTCAGAA 1174
QY 1021 TGGGAGGACAGCCCAAGCCACAGAGCCCTAGACACTGATGACCCCGAGCTGTAC 1080
Db 1175 TGGGAGGACAGTCCCAAGCCACAGAGCCCTAGACACTGATGACCCCGAGCTGTAC 1234
QY 1081 GCGGTGGTGGAGAACCTGCGCTGCGCTGGAAGAAATCGTGGCGCGCTTAGGGCTG 1140
Db 1235 GCGGTGGTGGAGAACCTGCGCTGCGCTGGAAGAAATCGTGGCGCGCTTAGGGCTG 1294
QY 1141 AGCAGCACAGATCGATCGGTGGAGCTGCGAGACGGCGCTGCTGCGGAGCGGCA 1200
Db 1295 AGCAGCACAGATCGATCGGTGGAGCTGCGAGACGGCGCTGCTGCGGAGCGGCA 1354
QY 1201 TACAGCATGCTGGGACCTGGAGGGCGGCGACGCGCGGAGCCAGCTGGAGCTG 1260
Db 1355 TACAGCATGCTGGGACCTGGAGGGCGGCGACGCGCGGAGCCAGCTGGAGCTG 1414
QY 1261 CTGGGACGCTGCTCCCGACATGGACCTGCTGGGCTGCTGGAGACATCGAGGAGCG 1320
Db 1415 CTGGGACGCTGCTCCCGACATGGACCTGCTGGGCTGCTGGAGACATCGAGGAGCG 1474
QY 1321 CTTTGGCGCCCGCCCTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 1368
Db 1475 CTTTGGCGCCCGCCCGCCCTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 1522
```

RESULT 15

AAQ12215

ID AAQ12215 standard; DNA; 2176 BP.

XX AC AAQ12215;

XX DT 12-SEP-1991 (first entry)

XX DE Type I TNF receptor.

XX KW Tumour Necrosis Factor; TNF; binding protein; TBP-I; ss.

XX OS Homo sapiens.

XX FH Key

XX FT terminator

XX Location/Qualifiers

XX 244..246

XX /tag= a

```
FT CDS /note= "in-frame termination codon"
FT /tag= a
FT /product= type I TNF receptor
FT /tag= b
FT /tag= c
FT /tag= d
FT /label= soluble_domain
FT /note= "may be 2 codons shorter or a few codons longer"
FT /tag= e
FT /note= "TBP-I derived sequence"
FT /tag= f
FT /note= "TBP-I derived sequence"
FT /tag= g
FT /note= "TBP-I derived sequence"
FT /tag= h
FT /label= transmembrane_domain
FT /tag= i
FT /number= 1
FT /tag= j
FT /number= 2
FT /tag= k
FT /number= 3
FT /tag= l
FT /number= 4
FT /tag= m
FT /tag= m
FT EP433900-A.
FT 26-JUN-1991.
FT 13-DEC-1990; 90BP-0124133.
FT 12-JUL-1990; 90IL-0095064.
FT 13-DEC-1989; 89IL-0092697.
FT (YEDA ) YEDA RES & DEV CO LTD.
FT Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
FT Aderka D;
FT WPI; 1991-186774/26.
FT P-PSDB; AARI2550.
FT Recombinant tumour necrosis factor binding protein I - prepd. by
FT transfecting eukaryotic cells with vector contg. deoxyribonucleic
FT acid encoding human type I TNF receptor or soluble domain
FT Disclosure; Fig 1(D); 30pp; English.
FT The Tumour Necrosis Factor Binding Protein I is the soluble form of
FT type I TNF-receptor and constitutes a fragment of the cell surface
FT form of this receptor, corresp. to its extracellular domain. 3' end
FT there is no characteristic poly(A) addition signal near the 3' end
FT of the cDNA. The sequence ACTAAA (tag m) may serve as an
FT alternative to this signal, but with low efficiency.
FT See also AAQ12212-15.
FT Sequence 2176 BP; 475 A; 644 C; 602 G; 455 T; 0 other;
FT
```

Query Match 99.6%; Score 1363.2; DB 12; Length 2176;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1365; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCCCTCTCCACCGTGCCTGACCTGCTGCTGCGACCTGGTGCCTCGAGCTGTGGTG 60
DB |||||||
QY 256 ATGGCCCTCTCCACCGTGCCTGACCTGCTGCTGCGCTGGTGCCTCGAGCTGTGGTG 315
DB |||||||
QY 61 GGAATATACCCCTCAGGCGTTTATGGACTGGTCCCTCACCTAGGGGACAGGGAGAGAGA 120
DB |||||||
QY 316 GGAATATACCCCTCAGGCGTTTATGGACTGGTCCCTCACCTAGGGGACAGGGAGAGAGA 375
DB |||||||
QY 121 GATAGTGTGTGCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGTGTAC 180
DB |||||||
QY 376 GATAGTGTGTGCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGTGTAC 435
DB |||||||
QY 181 AAGTGCCCAAGGAACTACTTGTACAAATGACTGTCCAGCGCCGGGACAGATACGGAC 240
DB |||||||
QY 436 AAGTGCCCAAGGAACTACTTGTACAAATGACTGTCCAGCGCCGGGACAGATACGGAC 495
DB |||||||
QY 241 TGCAGGGAGTGTGAGAGCGGCTCCTTTCACCGCTTCAGAAAAACCACTCAGACACTGCCTC 300
DB |||||||
QY 496 TGCAGGGAGTGTGAGAGCGGCTCCTTTCACCGCTTCAGAAAAACCACTCAGACACTGCCTC 555
DB |||||||
QY 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAGATCTCTTTCACAGTGGAC 360
DB |||||||
QY 556 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGTGGAGATCTCTTTCACAGTGGAC 615
DB |||||||
QY 361 CGGACACCGTGTGGCTGCAGGAAGAACAGTACCGGCATTTATGGAGTGAACCTT 420
DB |||||||
QY 616 CGGACACCGTGTGGCTGCAGGAAGAACAGTACCGGCATTTATGGAGTGAACCTT 675
DB |||||||
QY 421 TTCAGTGCCTCAATTTGAGCGCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 480
DB |||||||
QY 676 TTCAGTGCCTCAATTTGAGCGCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 735
DB |||||||
QY 481 AAACAGACACCGTGTGACCTGCCATGCCAGGTTTCTTCTAAGAGAAACAGTGTGTC 540
DB |||||||
QY 736 AAACAGACACCGTGTGACCTGCCATGCCAGGTTTCTTCTAAGAGAAACAGTGTGTC 795
DB |||||||
QY 541 TCCTGTAGTAACTGTAGAAAGCTGTGAGTGCACAGTGTGCTTACCCACAGATTGAG 600
DB |||||||
QY 796 TCCTGTAGTAACTGTAGAAAGCTGTGAGTGCACAGTGTGCTTACCCACAGATTGAG 855
DB |||||||
QY 601 AATGTTAAGGCACTGAGGACTCAGGCACACAGTGTGTTGCCCTGGTCAATTTCTTT 660
DB |||||||
QY 856 AATGTTAAGGCACTGAGGACTCAGGCACACAGTGTGTTGCCCTGGTCAATTTCTTT 915
DB |||||||
QY 661 GGTCTTTGCCCTTTATCCCTCTCTCTTCAATGGTTTAAATGTATCGCTACCAACGGTGGAG 720
DB |||||||
QY 916 GGTCTTTGCCCTTTATCCCTCTCTCTTCAATGGTTTAAATGTATCGCTACCAACGGTGGAG 975
DB |||||||
QY 721 TCCAAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGA 780
DB |||||||
QY 976 TCCAAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGA 1035
DB |||||||
QY 781 GGAATCTACTAAGCCCTCGGCCCAAAACCAAGCTTCAGTCCCACTCCAGGCTTCACC 840
DB |||||||
QY 1036 GGAATCTACTAAGCCCTCGGCCCAAAACCAAGCTTCAGTCCCACTCCAGGCTTCACC 1095
DB |||||||
QY 841 CCCACCTTGGGCTTCAGTCCCGTCCAGTTCACCTTCACCTCCAGCTCCACCTATACC 900
DB |||||||
QY 1096 CCCACCTTGGGCTTCAGTCCCGTCCAGTTCACCTTCACCTCCAGCTCCACCTATACC 1155
DB |||||||
QY 901 CCCGCTGACTGTCCCAACTTTGGGCTCCCGGACAGAGGTGGCACCACTATCAGGGG 960
DB |||||||
QY 1156 CCCGCTGACTGTCCCAACTTTGGGCTCCCGGACAGAGGTGGCACCACTATCAGGGG 1215
DB |||||||
QY 961 GCTGACCCCACTCTTGGGACAGCCCTCGCCTCCGACCCCACTCCCAACCCCTTCAGAAG 1020
DB |||||||
QY 1216 GCTGACCCCACTCTTGGGACAGCCCTCGCCTCCGACCCCACTCCCAACCCCTTCAGAAG 1275
DB |||||||
QY 1021 TGGGAGGACAGCGCCCAAGCCACAGAGCCTAGACACTGATGACCCCGGACCGCTGTAC 1080
DB |||||||

Search completed: June 8, 2003, 23:42:11
Job time : 348 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 8, 2003, 22:32:19 ; Search time 3520 Seconds
(without alignments)
11310.409 Million cell updates/sec

Title: US-09-899-422A-1

Perfect score: 1368

Sequence: 1 atgggcctctccacgtgcc.....cgccagctctctcagatga 1368

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.pat.*

23: em.ov.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rtd.*

36: em.htg.mam.*

37: em.htg.vrt.*

38: em.sy.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1368	100.0	1368	6	A29098	A29098 Synthetic D
2	1368	100.0	2112	9	HUMTNFR	M63121 Human tumor
3	1368	100.0	2194	9	BC010140	BC010140 Homo sapi
4	1366.4	99.9	2087	9	HUMTNFR	M33294 Human tumor
5	1366.4	99.9	2111	6	A26412	A26412 cDNA for (5
6	1366.4	99.9	2111	6	AX409713	AX409713 Sequence
7	1366.4	99.9	2111	9	HUMTNFR	M58286 Homo sapien
8	1366.4	99.9	2161	6	AR096330	AR096330 Sequence
9	1366.4	99.9	2161	9	HSTNFR1A	X55313 H.sapiens T
10	1366.4	99.9	2175	6	A43873	A43873 Sequence 1
11	1366.4	99.9	2175	6	A78738	A78738 Sequence 7
12	1366.4	99.9	2175	6	AR041076	AR041076 Sequence
13	1366.4	99.9	2175	6	I64751	I64751 Sequence 1
14	1366.4	99.9	2176	6	A19907	A19907 Synthetic n
15	1363.2	99.6	2062	6	A21522	A21522 TNF alpha q
16	1360	99.4	2062	6	I43805	I43805 Sequence 24
17	1351.2	98.8	2061	6	A20255	A20255 55KD recept
18	1344.4	98.3	2109	9	AK056611	AK056611 Homo sapi
19	1323.2	96.7	2050	9	HUMTNFR	M60275 Human tumor
20	1106	80.8	1331	6	A29103	A29103 H.sapiens m
21	890.6	65.1	2171	4	AB051103	AB051103 Felis cat
22	861	62.9	2004	4	SSU19994	U19994 Sus scrofa
23	743.4	54.3	2115	10	AF329976	AF329976 Rattus no
24	743.4	54.3	2115	10	AF329977	AF329977 Rattus no
25	743.4	54.3	2130	6	AX401925	AX401925 Sequence
26	743.4	54.3	2130	10	RATTNFR	M63122 Rat tumor n
27	741.8	54.2	2115	10	AF329978	AF329978 Rattus no
28	741.8	54.2	2115	10	AF329979	AF329979 Rattus no
29	741.8	54.2	2115	10	AF329980	AF329980 Rattus no
30	741.8	54.2	2115	10	AF329981	AF329981 Rattus no
31	690.4	50.5	1956	10	MUSTNFR2	M59377 Murine tumo
32	690.4	50.5	2048	10	MUSTNFR1	M60468 Mouse tumor
33	690.4	50.5	2063	10	MMP55R	X59238 Murine mRNa
34	690.4	50.5	2086	10	BC004599	BC004599 Mus muscu
35	690.4	50.5	2154	10	MUSTNFX	L26349 Mus musculu
36	690.4	50.5	2179	10	MMTNFR5	X57796 Mouse mRNa
37	685.4	50.1	2440	4	BTU90937	U90937 Bos taurus
38	632.8	46.3	6896	6	AR031375	AR031375 Sequence
39	632.8	46.3	6896	6	BD009743	BD009743 Compositi
40	632.4	46.2	6889	6	I26928	I26928 Sequence 2
41	596.8	43.6	600	6	A20257	A20257 Synthetic n
42	593.6	43.4	600	6	I43808	I43808 Sequence 47
43	514	37.6	1301	6	AR131310	AR131310 Sequence
44	514	37.6	1301	6	AR134762	AR134762 Sequence
45	510	37.3	510	6	A21525	A21525 oligonucleo

ALIGNMENTS

RESULT 1

A29098

LOCUS

DEFINITION

ACCESSION

VERSION

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

A29098 1368 bp DNA linear PAT 03-JUL-1995
Synthetic DNA for TNF-receptor from patent EP0393438.

A29098 GI:1248892

synthetic construct.

synthetic construct

artificial sequences.

1 (bases 1 to 1368)

Hauptmann,R., Himmeler,A., Maurer-Fogy,I. and Stratowa,C.

TNF-receptor, TNF-binding protein and DNA coding therefor

Patent: EP 0393438-A 48 24-OCT-1990;

BOEHRINGER INGELHEIM INTERNATIONAL G.M.B.H

Db	247	GGAAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGAGGACAGGAGAGAGA	306
QY	121	GATAGTGTGTGCCCAAGAAAAATATATCCACCTCAAAATTAATTCGATTGCTGTACC	180
Db	307	GATAGTGTGTGCCCAAGAAAAATATATCCACCTCAAAATTAATTCGATTGCTGTACC	366
QY	181	AAGTCCCAAGAGAACCTACTTGTACATGACTGTCCAGGCGCGGGGAGATACGGAC	240
Db	367	AAGTCCCAAGAGAACCTACTTGTACATGACTGTCCAGGCGCGGGGAGATACGGAC	426
QY	241	TGCAGGGAGTGTGAGAGCGGCTTCCTTCACCGCTTCAGAAAAACACTCAGACACTGCCTC	300
Db	427	TGCAGGGAGTGTGAGAGCGGCTTCCTTCACCGCTTCAGAAAAACACTCAGACACTGCCTC	486
QY	301	AGCTGCTCAAAATGCGGAAAGAAATGGGTGAGTGGAGATCTCTTCTTGCACAGTGGAC	360
Db	487	AGCTGCTCAAAATGCGGAAAGAAATGGGTGAGTGGAGATCTCTTCTTGCACAGTGGAC	546
QY	361	CGGGACACGCTGTGGCTGCAGGAGAACCACTACCGCATATTGGAGTCAAAACCTT	420
Db	547	CGGGACACGCTGTGGCTGCAGGAGAACCACTACCGCATATTGGAGTCAAAACCTT	606
QY	421	TTCCAGTGTCTCAATTCAGCGCTCTGCTCAATGGGACCGTGCACCTCTCTGCGCAGGAG	480
Db	607	TTCCAGTGTCTCAATTCAGCGCTCTGCTCAATGGGACCGTGCACCTCTCTGCGCAGGAG	666
QY	481	AAACAGACACGCTGTGCACCTGCATGAGGTTCTTTCTAAGAGAAACAGTGTGTC	540
Db	667	AAACAGACACGCTGTGCACCTGCATGAGGTTCTTTCTAAGAGAAACAGTGTGTC	726
QY	541	TCCTGTAGTAAGTAAAGAAAGCCTGGAGTGCAGAGTGTGCTTACCCAGATTGAG	600
Db	727	TCCTGTAGTAAGTAAAGAAAGCCTGGAGTGCAGAGTGTGCTTACCCAGATTGAG	786
QY	601	AATGTTAAGGACACTGAGGACTCAGGCACCACTGCTGTTGCCCTGCTCATTTCTTT	660
Db	787	AATGTTAAGGACACTGAGGACTCAGGCACCACTGCTGTTGCCCTGCTCATTTCTTT	846
QY	661	GGTCTTTGCTTTTATCCCTCTCTTCAATGTTTAAATGATCGCTACCAACGGTGGAG	720
Db	847	GGTCTTTGCTTTTATCCCTCTCTTCAATGTTTAAATGATCGCTACCAACGGTGGAG	906
QY	721	TCCAAGCTCTACTCATCTTTTGTGGAAATCGACACCTGAAAGAGGGGAGCTGAA	780
Db	907	TCCAAGCTCTACTCATCTTTTGTGGAAATCGACACCTGAAAGAGGGGAGCTGAA	966
QY	781	GGAACCTACTAAGCCCTTGCCGCCCAACCAAGCTTCAGTCCCACTCCAGCTTCACC	840
Db	967	GGAACCTACTAAGCCCTTGCCGCCCAACCAAGCTTCAGTCCCACTCCAGCTTCACC	1026
QY	841	CCACCCCTGGGCTTTCAGTCCGCTGCCAGTTCACCTTCACCTCCAGCTTCACCTATACC	900
Db	1027	CCACCCCTGGGCTTTCAGTCCGCTGCCAGTTCACCTTCACCTTCAGCTTCACCTATACC	1086
QY	901	CCCGGTGACTGTCCCAACTTTTCGGCTCCCGCCAGAGAGTGGCACCCCTATCAGGG	960
Db	1087	CCCGGTGACTGTCCCAACTTTTCGGCTCCCGCCAGAGAGTGGCACCCCTATCAGGG	1146
QY	961	GCTGACCCCATCTTTCGACAGCCCTTCGCTCCGACCCCATCCCAACCCCTTCAGAG	1020
Db	1147	GCTGACCCCATCTTTCGACAGCCCTTCGCTCCGACCCCATCCCAACCCCTTCAGAG	1206
QY	1021	TGGGAGGACAGCCGCACAAAGCCACAGAGCCCTAGACACTGTATGACCCCGGAGCTGTAC	1080
Db	1207	TGGGAGGACAGCCGCACAAAGCCACAGAGCCCTAGACACTGTATGACCCCGGAGCTGTAC	1266
QY	1081	GGCGTGTGGAGACCTGCCCCGTTGCGCTGGAAGAAATTCGTGGGCGCCTAGGGCTG	1140
Db	1267	GGCGTGTGGAGACCTGCCCCGTTGCGCTGGAAGAAATTCGTGGGCGCCTAGGGCTG	1326
QY	1141	AGCGACACAGATCATCGGTGGAGCTGCAGACGGCGCTGCTGCGCGGAGGGGCA	1200
Db	1327	AGCGACACAGATCATCGGTGGAGCTGCAGACGGCGCTGCTGCGCGGAGGGGCA	1386
QY	1201	TACAGCATCTGGCAGACCTGGAGGGCGCACCGCGCGGAGGCCACGCTGGAGCTG	1260
Db	1387	TACAGCATCTGGCAGACCTGGAGGGCGCACCGCGCGGAGGCCACGCTGGAGCTG	1446
QY	1261	CTGGGACGCTGCTCCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCAGAGGGG	1320
Db	1447	CTGGGACGCTGCTCCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCAGAGGGG	1506
QY	1321	CTTTGGGCGCGCGCGCTCCCGCGCGCGCGCTTCCTTCAGATGA	1368
Db	1507	CTTTGGGCGCGCGCGCTCCCGCGCGCGCGCTTCCTTCAGATGA	1554
RESULT 7			
HUMTNFRB			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
FEATURES			
source			
gene			
CDS			
Location/Qualifiers			
1..2111			
/organism="Homo sapiens"			
/db_xref="taxon:9606"			
/cell_line="HL60"			
1..2111			
/gene="TNF receptor"			
187..1554			
/gene="TNF receptor"			
/note="55 kDa"			
/codon_start=1			
/product="tumor necrosis factor receptor"			
/protein_id="AAA36753.1"			
/db_xref="GI:339754"			
/translation="MGLSVDPDLLPLVLELLVGYPSVIGLVPHLGDREKRSVC			
PGKYIHPONNSICCTKCHKGYLYNDGPGQDTCRECSGFTASNHLHCLSC			
SKCRKMGQVEISSCTVDRTVCGCKRNOYRHYWSENLFQCFNCISLNGTVHLSCQ			
KQNTVCTHAGFFLRNEKSCSNCKSLKCLPQIENYKGTDSGTLLPLVI			
FPLGLILSLFLGLMYRYQWKSKLYSIVCGKSTPEKELEGTTPKPLAPNPSPT			
PQFTPTLGSFVPSVSTTSSVTTGDCPNFAAPREVAPVPGADPILATASDPI			
NPILQKWDASHKPOSLLDPPDPAIVAVENVPPLRWKFEVRLGLSDHEIDRLQLN			
GCLREAOYSMLATWRRTPPRENTLEILLGRVLRDMDLLGCLIEALCGPALPPA			
PSLLR"			
187..273			
/gene="TNF receptor"			
274..1551			
/gene="TNF receptor"			
/product="tumor necrosis factor receptor"			
BASE COUNT			
ORIGIN			
445 a 629 c 587 g 450 t			
sig_peptide			
mat_peptide			
Query Match			
Best Local Similarity			
Matches 1367; Conservative			
99.9%; Score 1366.4; DB 9; Length 2111;			
99.9%; Pred. No. 2.1e-265;			
0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	ATGGGCTCTCCACCGTGGCTGACCTGCTGCTGCCACTGGTCTCCTCGGAGCTGTGGTG	60
Db	187	ATGGGCTCTCCACCGTGGCTGACCTGCTGCTGCCACTGGTCTCCTCGGAGCTGTGGTG	246
QY	61	GGAAATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGAGGACAGGAGAGA	120

QY 421 TTCCAGTGTTCATTAATGACGCTCTGCTCAATGGGACCGTGCACCTCTCTCTGCAGGAG 480
Db TTCCAGTGTTCATTAATGACGCTCTGCTCAATGGGACCGTGCACCTCTCTCTGCAGGAG 735
QY 481 AAACAGAACACCGTGTGACCTGCCATGCAGTCTTCTTCTTAAGAGAAACAGAGTGTCTC 540
- Db AAACAGAACACCGTGTGACCTGCCATGCAGTCTTCTTCTTAAGAGAAACAGAGTGTCTC 795
QY 541 TCCTGTAGTAACTGTAAAGAACGCTGGAGTGCAGAAAGTGTGTGCTACCCACAGATTGAG 600
Db TCCTGTAGTAACTGTAAAGAACGCTGGAGTGCAGAAAGTGTGTGCTACCCACAGATTGAG 855
QY 601 AATGTTAAGGACCTGAGGACTCAGGACACAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db AATGTTAAGGACCTGAGGACTCAGGACACAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCT 915
QY 661 GGTCTTTGCTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db GGTCTTTGCTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 975
QY 721 TCCAAAGCTCTACTCCATTTGTTGTGGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 780
Db TCCAAAGCTCTACTCCATTTGTTGTGGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 1035
QY 781 GGAAGTACTAAGCCCTGCGCCCAACCAAGCTTTCAGTCCCACTCCAGGCTTAC 840
Db GGAAGTACTAAGCCCTGCGCCCAACCAAGCTTTCAGTCCCACTCCAGGCTTAC 1095
QY 841 CCCACCTTGGGCTTCAGTCCCGTGGCCAGTTCACCTTTCACCTCCAGCTTACCTTAC 900
Db CCCACCTTGGGCTTCAGTCCCGTGGCCAGTTCACCTTTCACCTCCAGCTTACCTTAC 1155
QY 901 CCCGCTGACTGTCCCAACTTTGCGGCTCCCGCAGAGAGTGGCACCCCTATCAGGG 960
Db CCCGCTGACTGTCCCAACTTTGCGGCTCCCGCAGAGAGTGGCACCCCTATCAGGG 1215
QY 961 GCTGACCCCACTTTCGACAGCCCTCGCTCCGACCCCACTCCCAACCCCTTCAGAG 1020
Db GCTGACCCCACTTTCGACAGCCCTCGCTCCGACCCCACTCCCAACCCCTTCAGAG 1275
QY 1021 TGGAGGACAGCGCCCAACGCCACAGACCTAGACACTGATGACCCCGCAGCGTGTAC 1080
Db TGGAGGACAGCGCCCAACGCCACAGACCTAGACACTGATGACCCCGCAGCGTGTAC 1335
QY 1081 GCGTGTGGAGAGCTGCCCCGTTGCGCTGGAAGAAATTCGTGCGCGCGCTAGGGCTG 1140
Db GCGTGTGGAGAGCTGCCCCGTTGCGCTGGAAGAAATTCGTGCGCGCGCTAGGGCTG 1395
QY 1141 AGCGACACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCTGCGGAGCGCAA 1200
Db AGCGACACGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCTGCGGAGCGCAA 1455
QY 1201 TACAGCATGCTGGGACCTGGAGCGGCGCACCGCGCGCGGAGCCACGCTGAGAGCTG 1260
Db TACAGCATGCTGGGACCTGGAGCGGCGCACCGCGCGGAGCCACGCTGAGAGCTG 1515
QY 1261 CTGGAGCGGCTGCTCCGGACATGACCTGCTGCGCTGCGCTGCGGAGGACATCGAGAGCG 1320
Db CTGGAGCGGCTGCTCCGGACATGACCTGCTGCGCTGCGCTGCGGAGGACATCGAGAGCG 1575
QY 1321 CTTTGGCGCGCGCGCGCTCCCGCCCGCCAGCTCTTCTCAGATGA 1368
Db CTTTGGCGCGCGCGCGCTCCCGCCCGCCAGCTCTTCTCAGATGA 1623

RESULT 10
A43873
LOCUS A43873 2175 bp DNA linear PAT 06-MAR-1997
DEFINITION Sequence 1 from Patent EP0657536.
ACCESSION A43873
VERSION A43873.1 GI:2299022
KEYWORDS
SOURCE unidentified.

ORGANISM unidentified
REFERENCE 1 (bases 1 to 2175)
AUTHORS Wallach,D., Brackebusch,C., Varfolomeev,E. and Batkin,M.
TITLE proteases capable of shedding the soluble TNF-receptor and TNF-R
derived peptides and antibodies against the proteases inhibiting
the shedding
Patent: EP 0657536-A 1 14-JUN-1995;
JOURNAL YEDA RES & DEV (IL)
COMMENT Other publication ZA 9407962 951121
Other publication JP 7194376 950801
Other publication AU 7574294 950504
Other publication CA 2133872 950413.
FEATURES
Location/Qualifiers
1..2175
/organism="unidentified"
/db_xref="taxon:32644"
256..1623
/note="unnamed protein product"
/codon_start=1
/protein_id="CAA02771.1"
/db_xref="GI:2299023"
/translation="MGLSTVPDLLLPLVLELLVGLVPSGVIGLPHGLDREKRDVSC
POGKIHPQNNISICTKHKGTLYINDCPGPGQDTCRESGSFTASENLHRLCLSC
SKKREMGQVEISSCTVDRTVCGRKNQRYHWSENLFCNGLCLNGTVHLSCQ
KONTVCTHAGFIRENECVSCNCKLEKLPQIENKGTSTGTVLPLVQI
PFGCLLSLLFLGMYRQWRSKLYSIVCKSTPEKEGLEGTTPKPLADNPSPT
PGFTPLTGFSPVSPSTSTSSSTYPGCPNFAAPREVAIPPYQCADPTLATALASDPI
PNPLQKEDSAHKQSLDTPDPAITYAVVENVPPLRWKEFVRRLGLSDHEDRLLELON
GRCLREAQYSLMATWRRRTPREATLELLGLRLMDLLGLLEDIEALCGPALPPA
PSLR"
BASE COUNT 474 a 641 c 604 g 456 t
ORIGIN
Query Match 99.9%; Score 1366.4; DB 6; Length 2175;
Best Local Similarity 99.9%; Pred. No. 2.1e-265;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGGCTCTCCACCGTGCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Db ATGGGCTCTCCACCGTGCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
QY 61 GGAATATACCCCTCAGGGGTTATTGGAGTGTCTCTACCTAGGGGACAGGAGAGAGA 120
Db GGAATATACCCCTCAGGGGTTATTGGAGTGTCTCTACCTAGGGGACAGGAGAGAGA 375
QY 121 GATAGTGTGTGTCGCCAAGGAAATATATCCACCTCAAAATTAATTCGATTTGCTGTACC 180
Db GATAGTGTGTGTCGCCAAGGAAATATATCCACCTCAAAATTAATTCGATTTGCTGTACC 435
QY 181 AAGTGCCCAAGGAACCTACTTGTACAACTGCTGTCCAGGCCCGGGGACAGATACGGAC 240
Db AAGTGCCCAAGGAACCTACTTGTACAACTGCTGTCCAGGCCCGGGGACAGATACGGAC 495
QY 241 TGCAGGGAGTGTGAGAGCGGCTCTCTTACCCGTTTCAGAAAACCACTCAGACACTGCTC 300
Db TGCAGGGAGTGTGAGAGCGGCTCTCTTACCCGTTTCAGAAAACCACTCAGACACTGCTC 555
QY 301 AGCTGCTCCAAATGCCAAGGAAATGGGTGAGTGGAGATCTCTTCTTGCACAGTGGAC 360
Db AGCTGCTCCAAATGCCAAGGAAATGGGTGAGTGGAGATCTCTTCTTGCACAGTGGAC 615
QY 361 CGGACACCGTGTGTGGCTGCAGGAAGAACAGTACCGGCAATTAATGGAGTGAACACCTT 420
Db CGGACACCGTGTGTGGCTGCAGGAAGAACAGTACCGGCAATTAATGGAGTGAACACCTT 675
QY 421 TTCAGTGTCTCAATTCGAGCTCTGCTCAATGGGACCGTGCACCTCTCTCTGCCAGGAG 480
Db TTCAGTGTCTCAATTCGAGCTCTGCTCAATGGGACCGTGCACCTCTCTCTGCCAGGAG 735
QY 481 AAACAGAACACCGTGTGCACCTGCATGCAGTCTTCTTCTTAAGAGAAACAGAGTGTCTC 540
Db AAACAGAACACCGTGTGCACCTGCATGCAGTCTTCTTCTTAAGAGAAACAGAGTGTCTC 795

541 TCCTGTAGTAAGTAAAGAAAGCCGAGAGTGCACGAGTGTGGCTACCCAGATTGAG 600
|||||
796 TCCTGTAGTAAGTAAAGAAAGCCGAGAGTGCACGAGTGTGGCTACCCAGATTGAG 855
|||||
601 AATGTTAAGGACATGAGGACATGAGCAGCAGCAGTGTGCTGCTGCTGCTGCTGCTGCT 660
|||||
856 AATGTTAAGGACATGAGGACATGAGCAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 915
|||||
661 GGTCTTTGCTTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
|||||
916 GGTCTTTGCTTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 975
|||||
721 TCAAGCTCTACTCCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 780
|||||
976 TCAAGCTCTACTCCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1035
|||||
781 GGAACCTACTTAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
|||||
1036 GGAACCTACTTAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1095
|||||
841 CCCACCTGGGCTTCAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
|||||
1096 CCCACCTGGGCTTCAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1155
|||||
901 CCGGTGACTGTCCTCAACTTTGGGGTCCCGGAGAGAGTGGCACCCTTATCAGGGG 960
|||||
1156 CCGGTGACTGTCCTCAACTTTGGGGTCCCGGAGAGAGTGGCACCCTTATCAGGGG 1215
|||||
961 GTGACCCCATCTTCCGACAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
|||||
1216 GTGACCCCATCTTCCGACAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1275
|||||
1021 TGGAGGACAGCCGACCAAGCCACAGAGCCCTAGACACTGATGACCCCGGAGGCTGTAC 1080
|||||
1276 TGGAGGACAGCCGACCAAGCCACAGAGCCCTAGACACTGATGACCCCGGAGGCTGTAC 1335
|||||
1081 GCGGTGTTGAGAACGTGCCCCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
|||||
1336 GCGGTGTTGAGAACGTGCCCCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1395
|||||
1141 AGCGACACGAGATCGATCGCTGAGCTGACAGAGCCGCTGCTGCTGCTGCTGCTGCTGCT 1200
|||||
1396 AGCGACACGAGATCGATCGCTGAGCTGACAGAGCCGCTGCTGCTGCTGCTGCTGCTG 1455
|||||
1201 TACAGATGCTGCGACCTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1260
|||||
1456 TACAGATGCTGCGACCTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1515
|||||
1261 CTGGGACGCTGCTCCGCGACATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
|||||
1516 CTGGGACGCTGCTCCGCGACATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1375
|||||
1321 CTGTTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
|||||
1576 CTGTTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1623
|||||

RESULT 11

A78738
LOCUS A78738 2175 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 7 from Patent EP0568925.
ACCESSION A78738
VERSION A78738.1 GI:6090341
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2175)
AUTHORS Brakebusch, C. and Wallach, D.
TITLE TNF RECEPTOR ACTION MODULATION
JOURNAL Patent: EP 0568925-A 7 10-NOV-1993;
YEDA RES & DEV (11)

FEATURES
source
Location/Qualifiers
1. 2175
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 474 a 641 c 604 g 456 t
ORIGIN
Query Match 99.9%; Score 1366.4; DB 6; Length 2175;
Best Local Similarity 99.9%; Pred. No. 2.1e-265;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGGGCTCTCCACCGTGCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
|||||
Db 256 ATGGGGCTCTCCACCGTGCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
|||||
QY 61 GGAATATATACCCCTCAGGGGTATTGGACTGGTCCCTCAGCTAGGGGACAGGAGAGAGA 120
|||||
Db 316 GGNATATACCCCTCAGGGGTATTGGACTGGTCCCTCAGCTAGGGGACAGGAGAGAGA 375
|||||
QY 121 GATAGTGTGTGCCCAAGAAATATATCCACCTCAAAATAATTCGATTTGCTGTACC 180
|||||
Db 376 GATAGTGTGTGCCCAAGAAATATATCCACCTCAAAATAATTCGATTTGCTGTACC 435
|||||
QY 181 AAGTGGCCACAAAGGAACCTACTTGTACATGACTGTCCAGGCCCGGGGAGGATACGGAC 240
|||||
Db 436 AAGTGGCCACAAAGGAACCTACTTGTACATGACTGTCCAGGCCCGGGGAGGATACGGAC 495
|||||
QY 241 TGCAGGAGTGTGAGAGCGCTCTTCAACGCTTTCAGAAACCCACCTCAGACACTGCCTC 300
|||||
Db 496 TGCAGGAGTGTGAGAGCGCTCTTCAACGCTTTCAGAAACCCACCTCAGACACTGCCTC 555
|||||
QY 301 AGCTGTCCAAATGCCGAAAGAAATGGGTGAGGTGAGATCTCTTTTCACAGTGGAC 360
|||||
Db 556 AGCTGTCCAAATGCCGAAAGAAATGGGTGAGGTGAGATCTCTTTTCACAGTGGAC 615
|||||
QY 361 CGGGACACGCTGTGCTGCTGAGAGAACCTGACCTGACCTGCTGCTGCTGCTGCTGCTGCT 420
|||||
Db 616 CGGGACACGCTGTGCTGCTGAGAGAACCTGACCTGACCTGCTGCTGCTGCTGCTGCTGCT 675
|||||
QY 421 TTCCAGTGTCTCAATTTGCAGCCCTCTGCTCAATTTGGGACCGCTGACCTCTCTCTCCAGGAG 480
|||||
Db 676 TTCCAGTGTCTCAATTTGCAGCCCTCTGCTCAATTTGGGACCGCTGACCTCTCTCTCCAGGAG 735
|||||
QY 481 AAACAGAACACCGTGTGACCTGCCATGAGGTTTCTTCTAAGAGAAACAGAGTGTGTC 540
|||||
Db 736 AAACAGAACACCGTGTGACCTGCCATGAGGTTTCTTCTAAGAGAAACAGAGTGTGTC 795
|||||
QY 541 TCCCTGTAGTAAGTAAAGAAAGCCCTGAGTGCACGAGTGTGCTGCTGCTGCTGCTGCTGCT 600
|||||
Db 796 TCCCTGTAGTAAGTAAAGAAAGCCCTGAGTGCACGAGTGTGCTGCTGCTGCTGCTGCTGCT 855
|||||
QY 601 AATGTTAAGGACATGAGGACATGAGGACATGAGGACATGAGGACATGAGGACATGAGGAC 660
|||||
Db 856 AATGTTAAGGACATGAGGACATGAGGACATGAGGACATGAGGACATGAGGACATGAGGAC 915
|||||
QY 661 GGTCTTTGCTTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
|||||
Db 916 GGTCTTTGCTTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 975
|||||
QY 721 TCCAAGCTCTACTCCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 780
|||||
Db 976 TCCAAGCTCTACTCCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1035
|||||
QY 781 GGAACCTACTTAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
|||||
Db 1036 GGAACCTACTTAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1095
|||||
QY 841 CCCACCTGGGCTTCAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
|||||
Db 1096 CCCACCTGGGCTTCAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1155
|||||
QY 901 CCGGTGACTGTCCTCAACTTTGGGGTCCCGGAGAGAGTGGCACCCTTATCAGGGG 960
|||||

Db 1156 CCGGTGACTGTCCTCCAACTTTGGGGTCTCCCGCAGAGAGGTGGGACCAACCCCTATCAGGGG 1215
Qy 961 GCTGACCCCTCTTTGGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1020
Db 1216 GCTGACCCCTCTTTGGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTCAGAG 1275
Qy 1021 TGGAGGACAGCGGCCCAAGCCACAGACCTAGACACTGATGACCCCGGACGCTGTAC 1080
Db 1276 TGGAGGACAGCGGCCCAAGCCACAGACCTAGACACTGATGACCCCGGACGCTGTAC 1335
Qy 1081 GCCGTGTGGAGAACGTCGCCCTGCTGGAGGAATTCGTGGCGGCTAGGGCTG 1140
Db 1336 GCCGTGTGGAGAACGTCGCCCTGCTGGAGGAATTCGTGGCGGCTAGGGCTG 1395
Qy 1141 AGCACCACAGATCGATCGCTGGAGCTGCAGAACGGGCGCTGCCCTGCGGAGCGCAA 1200
Db 1396 AGCACCACAGATCGATCGCTGGAGCTGCAGAACGGGCGCTGCCCTGCGGAGCGCAA 1455
Qy 1201 TACAGCATGCTGGGACCTGGAGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1260
Db 1456 TACAGCATGCTGGGACCTGGAGCGGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1515
Qy 1261 CTGGAGCGCTGCTCGCGACATGGACCTGCTGGGCTGCCCTGGAGGACATCGAGAGCG 1320
Db 1516 CTGGAGCGCTGCTCGCGACATGGACCTGCTGGGCTGCCCTGGAGGACATCGAGAGCG 1575
Qy 1321 CTTTGGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
Db 1576 CTTTGGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1623

RESULT 12
AR041076 2175 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 1 from patent US 5811261.
DEFINITION AR041076
ACCESSION AR041076
VERSION AR041076.1 GI:5961572
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2175)
AUTHORS Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and Aderka,D.
TITLE Expression of the recombinant tumor necrosis factor binding protein I (TBP-I)
JOURNAL Patent: US 5811261-A 1 22-SEP-1998;
FEATURES Location/Qualifiers
source 1..2175
BASE COUNT 474 a 641 c 604 g 456 t
ORIGIN

Query Match 99.9%; Score 1366.4; DB 6; Length 2175;
Best Local Similarity 99.9%; Pred. No. 2.1e-265;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGGCGCTCTCCACCGCTGACCTGCTGCTGCGCACTGTGTCTCTGGAGCTGTGGTG 60
Db 256 ATGGGCGCTCTCCACCGCTGACCTGCTGCTGCGCGCTGTGTCTCTGGAGCTGTGGTG 315
Qy 61 GGAATATACCCCTCAGGGGTTATTGGACTGTGTCTCCCTCACCTAGGGGACAGGAGA 120
Db 316 GGAATATACCCCTCAGGGGTTATTGGACTGTGTCTCCCTCACCTAGGGGACAGGAGA 375
Qy 121 GATAGTGTGTGTCCTCCCAAGGAATATATCCACCCTCAAAATATTGATTTGCTGTACC 180
Db 376 GATAGTGTGTGTCCTCCCAAGGAATATATCCACCCTCAAAATATTGATTTGCTGTACC 435
Qy 181 AAGTGCCCAAAAGGAACCTACTTGTACAATGACTGTCTCAGGCCCGGGCGAGATACGGAC 240
Db 436 AAGTGCCCAAAAGGAACCTACTTGTACAATGACTGTCTCAGGCCCGGGCGAGATACGGAC 495

Qy 241 TGCAGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACTCAGACACTGCCTC 300
Db 496 TGCAGGAGTGTGAGAGCGGCTCTTTCACCGCTTCAGAAAACCACTCAGACACTGCCTC 555
Qy 301 AGCTGCTCCAAATCCGAAAGAAATGGGTGAGTGGAGATCTCTTCTTGACAGTGGAC 360
Db 556 AGCTGCTCCAAATCCGAAAGAAATGGGTGAGTGGAGATCTCTTCTTGACAGTGGAC 615
Qy 361 CGGACACCGCTGTGGCTGCAGGAAGAACCACTACCGGCATTTATTTGGAGTGAACCTT 420
Db 616 CGGACACCGCTGTGGCTGCAGGAAGAACCACTACCGGCATTTATTTGGAGTGAACCTT 675
Qy 421 TTCCAGTGTCTCAATTTGAGCCTCTGCCTCAATGGGACCGTGCACCTCTCTTCCAGAG 480
Db 676 TTCCAGTGTCTCAATTTGAGCCTCTGCCTCAATGGGACCGTGCACCTCTCTTCCAGAG 735
Qy 481 AAACAGAACACCGTGTGCACCTGCATGCAGGTTTCTTCTAAGNAGAAACGAGTGTCT 540
Db 736 AAACAGAACACCGTGTGCACCTGCATGCAGGTTTCTTCTAAGNAGAAACGAGTGTCT 795
Qy 541 TCCTGTAGTAACTGTAAAGAAAGCCTGGAGTGCACGAAGTTGTGCTTACCCAGATTGAG 600
Db 796 TCCTGTAGTAACTGTAAAGAAAGCCTGGAGTGCACGAAGTTGTGCTTACCCAGATTGAG 855
Qy 601 AATGTTAAGGCACTGAGGACTCAGGACACACAGTGTGTGCCCCCTGGTCACTTCTTT 660
Db 856 AATGTTAAGGCACTGAGGACTCAGGACACACAGTGTGTGCCCCCTGGTCACTTCTTT 915
Qy 661 GGTCTTTGGCCTTTATCCCTCCTCTCATTTGTTTAAATGATGATCGCTACCAACGTTG 720
Db 916 GGTCTTTGGCCTTTATCCCTCCTCTCATTTGTTTAAATGATGATCGCTACCAACGTTG 975
Qy 721 TCCAAGCTCTACTCCATTTGTTGGAAATTCGACACCTGAAAAGAGGGGAGCTTGAA 780
Db 976 TCCAAGCTCTACTCCATTTGTTGGAAATTCGACACCTGAAAAGAGGGGAGCTTGAA 1035
Qy 781 GGAATCTACTAAGCCCTCGGCCCAAAACCCAGTTCAGTCCCACTCCAGGCTTCACC 840
Db 1036 GGAATCTACTAAGCCCTCGGCCCAAAACCCAGTTCAGTCCCACTCCAGGCTTCACC 1095
Qy 841 CCCACCTTGGGCTTCAGTCCCGTCCGACCTTCCACCTTCACCTCCAGCTCCACCTATACC 900
Db 1096 CCCACCTTGGGCTTCAGTCCCGTCCGACCTTCCACCTTCACCTCCAGCTCCACCTATACC 1155
Qy 901 CCCGCTGACTCTCCCAACTTTTGGCGCTCCCGCAGAGAGGTGGCACCACTATCAGGG 960
Db 1156 CCCGCTGACTCTCCCAACTTTTGGCGCTCCCGCAGAGAGGTGGCACCACTATCAGGG 1215
Qy 961 GCTGACCCCATCTTGGGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTTCAGAG 1020
Db 1216 GCTGACCCCATCTTGGGACAGCCCTCGCTCCGACCCCATCCCAACCCCTTTCAGAG 1275
Qy 1021 TGGGAGGACAGCGCCCAAGCCACAGACCTAGACACTGATGATCCCGGACGCTGTAC 1080
Db 1276 TGGGAGGACAGCGCCCAAGCCACAGACCTAGACACTGATGATCCCGGACGCTGTAC 1335
Qy 1081 GCCGTGTGGAGAACGTCGCCCTTGGCTTGGAGGAATTCGTGCGCGCGCTAGGGCTG 1140
Db 1336 GCCGTGTGGAGAACGTCGCCCTTGGCTTGGAGGAATTCGTGCGCGCGCTAGGGCTG 1395
Qy 1141 AGCACCACAGATCGATCGCTGGAGCTGCAGAACCGGCGCTGCCCTGCGGAGCGCAA 1200
Db 1396 AGCACCACAGATCGATCGCTGGAGCTGCAGAACCGGCGCTGCCCTGCGGAGCGCAA 1455
Qy 1201 TACAGCATGCTGGGACCTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1260
Db 1456 TACAGCATGCTGGGACCTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1515
Qy 1261 CTGGAGCGCTGCTCCCGACATGGACCTGCTGGGCTGCCCTGGAGGACATCGAGAGCG 1320
Db 1516 CTGGAGCGCTGCTCCCGACATGGACCTGCTGGGCTGCCCTGGAGGACATCGAGAGCG 1575
Qy 1321 CTTTGGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368

Db

1576 CTTTGGGGCCCCGGCCCTCCCGCCGGCCAGTCTTCTCAGATGA 1623

RESULT 13

I64751	I64751	2175 bp	DNA	linear	PAT 07-OCT-1997
LOCUS	Sequence 1 from patent US 5665859.				
DEFINITION	I64751				
ACCESSION	I64751.1	GI:2481645			
VERSION					
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 2175)				
AUTHORS	Wallach,D., Brakebusch,C., Varfolomeev,E. and Batkin,M.				
TITLE	Molecules influencing the shedding of the TNF receptor, their preparation and their use				
JOURNAL	Patent: US 5665859-A 1 09-SEP-1997;				
FEATURES	Location/Qualifiers				
source	1. .2175				
BASE COUNT	474 a	641 c	604 g	456 t	
ORIGIN	/organism="unknown"				

```
Query Match      99.9%; Score 1366.4; DB 6; Length 2175;
Best Local Similarity 99.9%; Pred. No. 2.1e-265;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

[illegible]

Qy	661	GGTCTTTGGCCTTTTATCCCTCCTCTCTCAATGTTTAAATGTATCGCTACCAACGGTGGAAAG	720
Db	916	GGTCTTTGGCCTTTTATCCCTCCTCTCTCAATGTTTAAATGTATCGCTACCAACGGTGGAAAG	975
Qy	721	TCCAAGCTCTACTCCCAATGTTTGTGGGAAATCGACACCTCGAAAAAGAGGGGGAGCTTGAA	780
Db	976	TCCAAGCTCTACTCCCAATGTTTGTGGGAAATCGACACCTCGAAAAAGAGGGGGAGCTTGAA	1035
Qy	781	GGAACTACTACTTAAGGCCCTTGGGCCCCAAACCCCAAGGTTTCAGTCCCACCTCCAGGCTTCACC	840
Db	1036	GGAACTACTACTTAAGGCCCTTGGGCCCCAAACCCCAAGGTTTCAGTCCCACCTCCAGGCTTCACC	1095
Qy	841	CCACGCTGGGCTTCAGTCCGCTGCCAGTTCCACCTTCACCTTCACCTTCACCTTCACCTATACC	900
Db	1096	CCACGCTGGGCTTCAGTCCGCTGCCAGTTCCACCTTCACCTTCACCTTCACCTTCACCTATACC	1155
Qy	901	CCCGGTGACTGTCCCAACTTTGGGGCTCCCGCCAGAGAGGTGGCACCAACCTATCAGGGG	960
Db	1156	CCCGGTGACTGTCCCAACTTTGGGGCTCCCGCCAGAGAGGTGGCACCAACCTATCAGGGG	1215
Qy	961	GCTGACCCCATCCTTGGCAGAGCCCTGCCTCCGACCCCATCCCAACCCCTTCAGAAG	1020
Db	1216	GCTGACCCCATCCTTGGCAGAGCCCTGCCTCCGACCCCATCCCAACCCCTTCAGAAG	1275
Qy	1021	TGGGAGCAGACGCCCAACAGCCACAGAGCCTTAGACACTGATCACCCCGCGAGCGCTGTAC	1080
Db	1276	TGGGAGCAGACGCCCAACAGCCACAGAGCCTTAGACACTGATCACCCCGCGAGCGCTGTAC	1335
Qy	1081	GCGGTGGTGAGAACGTGCCCCGTTTGCCTGTGGAAGGAATTCGTGGCGGCCCTTAGGGCTG	1140
Db	1336	GCGGTGGTGAGAACGTGCCCCGTTTGCCTGTGGAAGGAATTCGTGGCGGCCCTTAGGGCTG	1395
Qy	1141	AGCGACCAACAGAGATCGATCGGCTGGAGCTGCAGAAAGGGGCGCTGCCTGCGCAGAGGCGCAA	1200
Db	1396	AGCGACCAACAGAGATCGATCGGCTGGAGCTGCAGAAAGGGGCGCTGCCTGCGCAGAGGCGCAA	1455
Qy	1201	TACAGCATGCTGGGACCTTGAGGGCGCAGACGCCGGGCGCAGGCCACGCTTGGAGCTG	1260
Db	1456	TACAGCATGCTGGGACCTTGAGGGCGCAGACGCCGGGCGCAGGCCACGCTTGGAGCTG	1515
Qy	1261	CTGGGAGCGCTGTCTCCGCGACATGGACCTGCTGGGCTGCCTTGGAGGACATCGCAGGAGGCG	1320
Db	1516	CTGGGAGCGCTGTCTCCGCGACATGGACCTGCTGGGCTGCCTTGGAGGACATCGCAGGAGGCG	1575
Qy	1321	CTTTTGGGGCCCCCGCCCTTCCGCGCCCGCCAGTCTTCTCAGATGA	1368
Db	1576	CTTTTGGGGCCCCCGCCCTTCCGCGCCCGCCAGTCTTCTCAGATGA	1623

RESULT 14

AL19007	LOCUS	AL19007	2176 bp	DNA	linear	PAT 04-OCT-1994
	DEFINITION	Synthetic nucleotide sequence Type I TNF receptor gene.				
	ACCESSION	AL19007				
	VERSION	AL19007.1	GI:641222			
	KEYWORDS	synthetic construct.				
	SOURCE	synthetic construct				
	ORGANISM	artificial sequences.				
	REFERENCE	1 (bases 1 to 2176)				
	AUTHORS	Wallach,D., Nophar,Y., Kemper,O., Engelmann,H., Brakebusch,C. and Adgera,D.				
	TITLE	Expression of the recombinant tumor necrosis factor binding protein I (TBP-1)				
	JOURNAL	Patent: EP 0433900-A 28 JUN-1991;				
		YEDA RESEARCH AND DEVELOPMENT COMPANY LIMITED				
	FEATURES	Location/Qualifiers				
	SOURCE	1..2176				
		/organism="synthetic construct"				
		/db_xref="taxon:32630"				
	BASE COUNT	474 a	642 c	604 g	456 t	
	ORIGIN					

Query Match		99.9%; Score 1366.4; DB 6; Length 2176;
Best Local Similarity		99.9%; Pred. No. 2.1e-265;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1	ATGGGCTCTCCACCGTCCCTGACCTGCTGCTGCGCACTGGTGCCTCGGAGCTGTGGTG 60
DB	256	ATGGGCTCTCCACCGTCCCTGACCTGCTGCTGCGCTGGTGTCTCTCGGAGCTGTGGTG 315
QY	61	GGAATATACCCCTCAGGGGTTATTGGACTGGTGCCTCACCCTAGGGGACAGGAGAAGA 120
DB	316	GGAATATACCCCTCAGGGGTTATTGGACTGGTGCCTCACCCTAGGGGACAGGAGAAGA 375
QY	121	GATAGTGTGTGTCGCCAAGGAATATATCCACCTCAAAATATTGATTTGTGTACC 180
DB	376	GATAGTGTGTGTCGCCAAGGAATATATCCACCTCAAAATATTGATTTGTGTACC 435
QY	181	AAGTGCCCAAGGAACCTACTTGTACAATGACTGTCAGGCCGGGCGAGATACGGAC 240
DB	436	AAGTGCCCAAGGAACCTACTTGTACATGACTGTCCAGGCCGGGCGAGATACGGAC 495
QY	241	TGCAGGAGTGTGAGCGGCTCCTTCAACGGCTTCAGAAAACACCTCAGACACTGCCTC 300
DB	496	TGCAGGAGTGTGAGCGGCTCCTTCAACGGCTTCAGAAAACACCTCAGACACTGCCTC 555
QY	301	AGCTGCTCCCAATCCGAAAGAAATGGTCAGGTGGAGATCTCTTTCGCACAGTGGAC 360
DB	556	AGCTGCTCCCAATCCGAAAGAAATGGTCAGGTGGAGATCTCTTTCGCACAGTGGAC 615
QY	361	CGGACACCGTGTGGCTGCAGGAAGAACCAAGTACCGGCAATATTGGAGTGAACCTT 420
DB	616	CGGACACCGTGTGGCTGCAGGAAGAACCAAGTACCGGCAATATTGGAGTGAACCTT 675
QY	421	TTCAGTGTCTCAATTCAGCGCTCTGCTCAATGGGACCGTGCACCTCTCTGCGCAGG 480
DB	676	TTCAGTGTCTCAATTCAGCGCTCTGCTCAATGGGACCGTGCACCTCTCTGCGCAGG 735
QY	481	AAACAGAACCCGTGTGCACCTGCATGCAGGTTTCTTCTAAGAAAGACAGTGTGTC 540
DB	736	AAACAGAACCCGTGTGCACCTGCATGCAGGTTTCTTCTAAGAAAGACAGTGTGTC 795
QY	541	TCCTGTAGTAACTAAGAAAGCCTGGAGTGCACGAAGTTGTGCTTACCCACAGATTGAG 600
DB	796	TCCTGTAGTAACTAAGAAAGCCTGGAGTGCACGAAGTTGTGCTTACCCACAGATTGAG 855
QY	601	AATGTTAAGGCACCTGAGGACTCAGGACCAACAGTGTGTGCCCCCTGGTCATTTCTTT 660
DB	856	AATGTTAAGGCACCTGAGGACTCAGGACCAACAGTGTGTGCCCCCTGGTCATTTCTTT 915
QY	661	GGTCTTGGCCCTTTATCCCTCTCTTCAATGGTTTAAATGATCGCTACCAACGGTGAAG 720
DB	916	GGTCTTGGCCCTTTATCCCTCTCTTCAATGGTTTAAATGATCGCTACCAACGGTGAAG 975
QY	721	TCCAAGCTCTACTCCATTTGTTGGAAATCGACACCTGAAAAGAGGGGAGCTTGAA 780
DB	976	TCCAAGCTCTACTCCATTTGTTGGAAATCGACACCTGAAAAGAGGGGAGCTTGAA 1035
QY	781	GGAACCTACTAAGCCCTTGCCGCCAAACCCCAAGCTTCAGTCCCACTCCAGGCTTACC 840
DB	1036	GGAACCTACTAAGCCCTTGCCGCCAAACCCCAAGCTTCAGTCCCACTCCAGGCTTACC 1095
QY	841	CCCACCTCTGGCTTCAGTCCCGTCCAGTTCACCTTCACCTTCACCTTCACCTATACC 900
DB	1096	CCCACCTCTGGCTTCAGTCCCGTCCAGTTCACCTTCACCTTCACCTTCACCTATACC 1155
QY	901	CCCGGTGACTGTCCCAACTTTGGGGTCCCGCGCAGAGAGTGGCACACCCCTATCAGGG 960
DB	1156	CCCGGTGACTGTCCCAACTTTGGGGTCCCGCGCAGAGAGTGGCACACCCCTATCAGGG 1215
QY	961	GCTGACCCCATCTTGGCAGACCCCTCGCTCCGACCCCATCCCCACACCCCTTCAGAAG 1020
DB	1216	GCTGACCCCATCTTGGCAGACCCCTCGCTCCGACCCCATCCCCACACCCCTTCAGAAG 1275
QY	1021	TGGGAGACAGCGGCCCAAGCCACAGAGCTAGACACTGATGACCCCGCGACGCTGTAC 1080
Query Match		99.6%; Score 1363.2; DB 6; Length 2062;
Best Local Similarity		99.8%; Pred. No. 9.3e-265;
Matches 1365; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
QY	1	ATGGGCTCTCCACCGTCCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
DB	155	ATGGGCTCTCCACCGTCCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 214
QY	61	GGAATATACCCCTCAGGGGTTATTGGACTGGTGCCTCACCCTAGGGGACAGGAGAAGA 120
DB	215	GGAATATACCCCTCAGGGGTTATTGGACTGGTGCCTCACCCTAGGGGACAGGAGAAGA 274
QY	121	GATAGTGTGTGTCGCCAAGGAATATATCCACCTCAAAATATTGATTTGTGTACC 180
BASE COUNT		429 a 617 c 573 g 443 t
ORIGIN		
LOCUS		2062 bp mRNA linear PAT 26-JUL-1994
DEFINITION		TNF alpha gene.
ACCESSION		A21522
VERSION		A21522.1 GI:579599
KEYWORDS		Homo sapiens.
SOURCE		Homo sapiens
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
LOCATION/Qualifiers		Mammalia; Primates; Catarrhini; Homidae; Homo.
FEATURES		Location/Qualifiers
source		1..2062
gene		/organism="Homo sapiens"
CDS		/db_xref="taxon:9606"
		155..1522
		/gene="TNF alpha gene"
		155..1522
		/gene="TNF alpha gene"
		/codon_start=1
		/protein_id="CAA01558.1"
		/db_xref="GI:579600"
		/translation="MGLSTVPLDLLPLVLELVGIVPSGIVGLVPHLGRKRSVC
		POKYLHPONNSICTCKHGTLYNDPCPGODTDCRECEGSFTASENHLRCLSC
		SKRKEMQVEISCTVDRTVCGRKNOYRHWSENLFCQFNCSCLENGTVHLSCOE
		KQNTVCTCHAGFFLRENECVSCNKSLECKLCLPQIENVKGTDSGTVLLPLVI
		FFGLCLSLFLFGLMTRYQRMKSLYSIVCGKSTPEKELEGTTTKPLAPNPSFPT
		PGFTPTLGFSPVSPSTSTSTPGCPNFAAPRREVPYQCADPILATALASDPI
		PNPQKWEDESAHKQSLDTPDPAVLAVENVPPLRWKEFVRRLGSLDRLQLQ
		GRCLRQAQYSLMATEWRRTPREATLELLGRVLRDMLLCLLEIEALCGPALPFA
		PSLLR"

Db	275	GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATATTCGATTTCTGTAC	334
QY	181	AAGTGCCCAAGGAACTTACTTGTACAAATGACTGTCCAGGCGCGGGGAGGATACGGAC	240
Db	335	AAGTGCCCAAGGAACTTACTTGTACAAATGACTGTCCAGGCGCGGGGAGGATACGGAC	394
QY	241	TGCAGGGAGTGTGAGAGCGGCTTCTTACCGGCTTCAGAAACCACTCAGACACATGCCCTC	300
Db	395	TGCAGGGAGTGTGAGAGCGGCTTCTTACCGGCTTCAGAAACCACTCAGACACATGCCCTC	454
QY	301	AGCTGCTCCAAATGCGGAAAGAAATGGGTGAGTGGAGATCTCTTTGACAGTGGAC	360
Db	455	AGCTGCTCCAAATGCGGAAAGAAATGGGTGAGTGGAGATCTCTTTGACAGTGGAC	514
QY	361	CGGGACACCGTGTGGCTGCGAGGAGAACCACTACCGGCATATTGGAGTGAACACCTT	420
Db	515	CGGGACACCGTGTGGCTGCGAGGAGAACCACTACCGGCATATTGGAGTGAACACCTT	574
QY	421	TTCCAGTGTCTCAATTCAGCCCTCTGCCCTCAATGGACCGTGCACCTCTCTGCCAGGAG	480
Db	575	TTCCAGTGTCTCAATTCAGCCCTCTGCCCTCAATGGACCGTGCACCTCTCTGCCAGGAG	634
QY	481	AAACAGACACCGTGTGCACCTGCCATGACGCTTTCTTTCTAAGAGAAACAGTGTGTC	540
Db	635	AAACAGACACCGTGTGCACCTGCCATGACGCTTTCTTTCTAAGAGAAACAGTGTGTC	594
QY	541	TCCTGTAGTAACTGAAGAAAGCCTGGAGTGCACGAAAGTTGTGCTACCCAGATTTGAG	600
Db	695	TCCTGTAGTAACTGAAGAAAGCCTGGAGTGCACGAAAGTTGTGCTACCCAGATTTGAG	754
QY	601	AATGTTAAGGGCAGTGAAGAACTCAGGCACCACTGCTGTGCCCCGTGCTCAATTTCTTTT	560
Db	755	AATGTTAAGGGCAGTGAAGAACTCAGGCACCACTGCTGTGCCCCGTGCTCAATTTCTTTT	814
QY	661	GGTCTTTGCTTTTATCCCTCTCTTCAATGTTGTTTAAATGATGCTTACCAACGGTGAAG	720
Db	815	GGTCTTTGCTTTTATCCCTCTCTTCAATGTTGTTTAAATGATGCTTACCAACGGTGAAG	874
QY	721	TCCAAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGA	780
Db	875	TCCAAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGA	934
QY	781	GGAAGTACTACTAAGCCCTGCGCCCAACCAAGCTTCAGTCCCACTCCAGGCTTCACC	840
Db	935	GGAAGTACTACTAAGCCCTGCGCCCAACCAAGCTTCAGTCCCACTCCAGGCTTCACC	994
QY	841	CCACCCCTGGGCTTCAGTCCCGTGGCCAGTTCACCTTCACCTCCAGCTCCACCTATACC	900
Db	995	CCACCCCTGGGCTTCAGTCCCGTGGCCAGTTCACCTTCACCTCCAGCTCCACCTATACC	1054
QY	901	CCCGGTGACTGCCCAACTTTGCGGCTCCCGCAGAGAGTGGCACCCCTATCAGGGG	960
Db	1055	CCCGGTGACTGCCCAACTTTGCGGCTCCCGCAGAGAGTGGCACCCCTATCAGGGG	1114
QY	961	GCTGACCCCATCTTGGACAGCCCTCGGCTCGGACCCCATCCCAACCCCTTCAGAG	1020
Db	1115	GCTGACCCCATCTTGGACAGCCCTCGGCTCGGACCCCATCCCAACCCCTTCAGAG	1174
QY	1021	TGGGAGGACAGCGCCACAAAGCCACAGAGCTAGACACTGATGACCCCGGACGCTGTAC	1080
Db	1175	TGGGAGGACAGTGGCCACAAAGCCACAGAGCTAGACACTGATGACCCCGGACGCTGTAC	1234
QY	1081	GCCGTGGTGGAGACGTGCCCGGCTTGGCTGGAAGAAATCGTGGCGGCTTAGGGCTG	1140
Db	1235	GCCGTGGTGGAGACGTGCCCGGCTTGGCTGGAAGAAATCGTGGCGGCTTAGGGCTG	1294
QY	1141	ACGGACACAGATCGATCGGCTGGAGCTGCAGAACGGCGCTGCTGCGGAGGCGCAA	1200
Db	1295	ACGGACACAGATCGATCGGCTGGAGCTGCAGAACGGCGCTGCTGCGGAGGCGCAA	1354
QY	1201	TACAGCATGCTGGGACCTGGAGGGCGGCGCACCGCGGCGGACGCTGGAGCTG	1260
Db	1355	TACAGCATGCTGGGACCTGGAGGGCGGCGCACCGCGGCGGACGCTGGAGCTG	1414

QY	1261	CTGGGACGGGTGCTCCGCGACATGGACCTGCTGGGCTGCTGGAGACATCGAGAGGCG	1320
Db	1415	CTGGGACGGGTGCTCCGCGACATGGACCTGCTGGGCTGCTGGAGACATCGAGAGGCG	1474
QY	1321	CTTTGGGGCCCGCGCCCTCCCGCCGCGGCGCCAGTCTTCTCAGATGA	1368
Db	1475	CTTTGGGGCCCGCGCCCTCCCGCCGCGGCGCCAGTCTTCTCAGATGA	1522

Search completed: June 9, 2003, 01:12:25
Job time : 3526 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2003, 01:12:29 ; Search time 1566 Seconds
(without alignments)
4705.585 Million cell updates/sec

Title: US-09-899-422A-2

Perfect score: 2487

Sequence: 1 MGLSTVPDLLPLVLELLV.....DIEEALCGAALPPAPSLLR 455

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=slp
-Q/cgn2-1/USPTO.spool/US09899422/runat_04062003_145737_14712/app_query.fasta_1.647
-DB=EST -OPMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR=SCORE=pcr -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09899422.ecgn_1_1_2874_@runat_04062003_145737_14712 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPOP=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estnu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rtd: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1536	61.8	931	14	BQ723672	BQ723672 AGENCECOURT
2	1416	56.9	957	9	AL559050	AL559050 AL559050
3	1414	56.9	1076	14	BM923204	BM923204 AGENCECOURT
4	1292	52.0	741	13	BI860918	BI860918 603396284
5	1271.5	51.1	1070	13	BM546826	BM546826 AGENCECOURT
6	1268	51.0	761	9	AU131978	AU131978 AU131978
7	1261	50.7	942	9	AL529836	AL529836 AL529836
8	1245.5	50.1	975	9	AL577008	AL577008 AL577008
9	1234	49.6	974	12	BG180101	BG180101 602329676
10	1211.5	48.7	994	14	BM800044	BM800044 AGENCECOURT
11	1206	48.5	889	9	AU117362	AU117362 AU117362
12	1202	48.3	916	13	BI757305	BI757305 603029519
13	1195.5	48.1	718	12	BG680679	BG680679 602636965
14	1194	48.0	669	14	BM742388	BM742388 K-EST0015
15	1191	47.9	837	9	AL522989	AL522989 AL522989
16	1167	46.9	696	14	BM898994	BM898994 UI-H-DIO-
17	1152	46.3	818	13	BI821169	BI821169 603035068
18	1149.5	46.2	969	12	BE871809	BE871809 601448388
19	1126.5	45.3	859	13	BI870917	BI870917 603394462
20	1113	44.8	636	12	BG03257	BG03257 602324771
21	1113	44.8	1131	13	BM467058	BM467058 AGENCECOURT
22	1110.5	44.7	761	12	BG282718	BG282718 602406578
23	1108.5	44.6	769	9	AL522226	AL522226 AL522226
24	1096.5	44.1	872	13	BI769006	BI769006 603058164
25	1074	43.2	643	12	BG680356	BG680356 602629252
26	1071.5	43.1	602	14	BM791206	BM791206 K-EST0071
27	1070.5	43.0	627	14	BM763879	BM763879 K-EST0045
28	1063.5	42.8	845	9	AU125021	AU125021 AU125021
29	1056	42.5	575	14	BM705174	BM705174 UI-E-CIL-
30	1055	42.4	872	14	BQ723589	BQ723589 AGENCECOURT
31	1052	42.3	1008	14	BQ179773	BQ179773 AGENCECOURT
32	1048	42.1	859	9	AU124446	AU124446 AU124446
33	1046	42.1	767	9	AU142156	AU142156 AU142156
34	1037	41.7	576	14	BM820201	BM820201 K-EST0088
35	1037	41.7	936	12	BG681438	BG681438 602628106
36	1034.5	41.6	971	12	BE876920	BE876920 601488490
37	1028	41.3	811	12	BF342334	BF342334 602013123
38	1017	40.9	772	9	AU137990	AU137990 AU137990
39	1015.5	40.8	823	13	BI766980	BI766980 603054065
40	1010.5	40.6	929	12	BG677121	BG677121 602623792
41	1004	40.4	951	14	BQ882704	BQ882704 AGENCECOURT
42	996.5	40.1	915	14	BQ881180	BQ881180 AGENCECOURT
43	995.5	40.0	739	13	BI520191	BI520191 603071439
44	991	39.8	913	14	BQ926409	BQ926409 AGENCECOURT
45	985	39.6	817	9	AU125680	AU125680 AU125680

ALIGNMENTS

RESULT 1
BQ723672
LOCUS BQ723672 931 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCECOURT_8489850_lupski_dorsal_root_ganglion Homo sapiens cdna
clone IMAGE:6184295 5', mRNA sequence.
ACCESSION BQ723672
VERSION BQ723672.1 GI:21862569
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 931)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

**JOURNAL
COMMENT**

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cspbos-re@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAMI3573 row: d column: 24
High quality sequence stop: 607.

FEATURES
source

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone IMAGE:6184295"
/clone_lib=Lupski_dorsal_root_ganglion"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/notes="vector: pCMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: SalI; CDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACCGCTCCG-3' and
5'-GACGAGTCTCAGATCGAGCGCGCCTT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
218 a 283 c 224 g 204 t 2 others

```



```

Db      314 TTCAGTCCCGTCCGAGGTCACCTTCCAGCTCCAGCTCCAGCTATATACCCCGGTCACGT 373
Qy      305 ProAnPheAlaAlaProArgArgGluValAlaProProTyGInGInValAlaAspProfile 324
Db      374 CCCAACTTGGCGGTCCCGCAGAGAGGTGGACACACCTATCAGGGGGCTGACCCCATC 433
Qy      325 LeuAlaThrAlaLeuAlaSerAspProfileProAnPheProLeuGInLysTrpGluAspSer 344
Db      434 CTGGCAGAGCCCTCGCCTCCGAGCCCATCCCAACCCCTTCAAGAGTGGGAGACAGC 493
Qy      345 AlaHisLysProGInSerLeuAspThrAspAspProAlaThrLeuTyAlaValValGlu 364
Db      494 GCCCAACACCCACAGAGCTAGACACTGATGACCCCGGAGCGCTAGCCCGGTGGAG 553
Qy      365 AsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeuSerAspHisGlu 384
Db      554 AACGTGCCCGCTTGGCGCTGGAAGGAATTCTGCGGGCGCTAGGGCTGAGGACACAGAG 613
Qy      385 IleAspArgLeuGluLeuGInAsnGlyArgCysLeuArgGluAlaGlnTySerMetLeu 404
Db      614 ATCATCGGCTGGAGCTGCAGAACGGCGCTGCCCTGCGGAGGCGCAATACAGCATGCTG 673
Qy      405 AlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeuGlyArgVal 424
Db      674 CGACCTGGAGCGGCGGCACCCCGCGCGGAGCGCTGGAGCTCTGGAGCGCTG 733
Qy      425 LeuArgAspMetAspLeuLeuGlyCysLeuGluAspLysGluAlaLeuCysGlyPro 444
Db      734 CTCGCGACATGGACCTCTGGCTGCTGGGAGCATCGAGGANGCGCTTTGGCCCCC 793
Qy      445 AlaAlaLeuProProAlaProSerLeuLeuArg 455
Db      794 GNCGCCCTTCCGCGCGCGCCAGCTCTCTCAGA 826

```

RESULT 4

```

BI860918 741 bp mRNA linear EST 10-OCT-2001
LOCUS 603390284F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5399108 5',
DEFINITION mRNA sequence.

```

```

ACCESSION BI860918
VERSION BI860918.1 GI:16001653

```

```

KEYWORDS EST.

```

```

SOURCE human.

```

```

ORGANISM Homo sapiens

```

```

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

TITLE NIH-MGC http://mgi.nhl.gov/.

```

```

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

```

```

COMMENT Unpublished (1999)

```

```

Contact: Robert Strausberg, Ph.D.

```

```

Email: cgapbs-r@mail.nih.gov

```

```

Tissue Procurement: DCPD/BTP

```

```

cDNA Library Preparation: Life Technologies, Inc.

```

```

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

```

```

Clone distribution: MGC clone distribution information can be

```

```

found through the I.M.A.G.E. Consortium/LLNL at:

```

```

http://image.llnl.gov

```

```

Plate: L14M12017 row: h column: 21

```

```

High quality sequence stop: 740.

```

```

Location/Qualifiers

```

FEATURES

```

source

```

```

1..741

```

```

/organism="Homo sapiens"

```

```

/db_xref="taxon:9606"

```

```

/clone="IMAGE:5399108"

```

```

/tissue_type="mammary adenocarcinoma, cell line"

```

```

/lab_host="DH10B (phage-resistant)"

```

```

/note="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;

```

```

Site 2: SalI; Cloned unidirectionally; oligo-dt primed.

```

```

Average insert size 1.383 kb. Library enriched for

```

```

full-length clones and constructed by Life Technologies.

```

```

BASE COUNT 167 a Note: this is a NIH_MGC Library.

```

```

ORIGIN 229 c 175 g 170 t

```

Alignment Scores:

```

Pred. No.: 7.89e-114 Length: 741

```

```

Score: 1292.00 Matches: 241

```

```

Percent Similarity: 98.78% Conservative: 1

```

```

Best Local Similarity: 98.37% Mismatches: 2

```

```

Query Match: 51.95% Indels: 2

```

```

DB: 13 Gaps: 0

```

```

US-09-899-422a-2 (1-455) x BI860918 (1-741)

```

```

Qy      87 GlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeuSerCysSerLysCysArg 106
Db      3 GGCTCCTTCACCGCTTCAGAAAACACCTCAGACACTGCCTCAGCTGCTCCAAATGCCGA 62
Qy      107 LysGluMetGlyGInValGluIleSerSerCysThrValAspArgAspThrValCysGly 126
Db      63 AAGAAATGGGTCAAGTGGAGATCTCTTTCACAGTGGACCGGACACCGTGTGTGGC 122
Qy      127 CysArgLysAsnGInTyrArgHisTyrTrpSerGluAsnLeuPheGlnCysPheAsnCys 146
Db      123 TGCAGGAAGAACCACTACCGGCATATTGGAGTGAACACCTTTTCCAGTGTCTCAATTGC 182
Qy      147 SerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCys 166
Db      183 AGCCTCTGCCCTCATGGGACCGTGCACCTCTCTCCGAGGAGAAACAGAACACCGTGTGC 242
Qy      167 ThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerAsnCysLys 186
Db      243 ACCTGCCATGCAGGTTCTTTTAAAGAAAAACGAGTGTCTCTCTGTAGTAACCTGTAAAG 302
Qy      187 LysSerLeuGluCysThrLysLeuCysLeuProGlnIleGluAsnValLysGlyThrGlu 206
Db      303 AAAAGCCTGGAGTCACGAGATTTGTGCTACCCAGATTGAGAATGTTAAGGGCACTGAG 362
Qy      207 AspSerGlyThrThrValLeuProLeuValIlePhePheGlyLeuCysLeuSer 226
Db      363 GACTCAGGCACCAAGTGTCTTGCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 422
Qy      227 LeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLysSerLysLeuTyrSerIle 246
Db      423 CTCCTCTCTATTGTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 482
Qy      247 ValCysGlyLysSerThrProGluLysGluGluGluGluGluGluGluGluGluGluGlu 266
Db      483 GTTTGTGGGAATGCACACCTGAAAAGAGAGGGGAGGCTTGAAGGAACCTACTACTAAGCC 542
Qy      267 LeuAlaProAnProSerPheSerProThrProGlyPheThrProThrLeuGlyPheSer 286
Db      543 CTGCCCCCAACCAACCAAGCTTCAGTCCACCTCCAGCTTCACCCCACTCCGGGCTTCAGT 602
Qy      287 ProValProSerSerThrPheThrSerSerSerThrThrThrProGlyAspCysProAn 306
Db      603 CCCGTGCCAGTTCACCTTCACCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCTCCAGCT 662
Qy      307 PheAlaAlaProArgArgGluValAlaProProTyrGln-GlyAlaAlaProIleLeuAl 326
Db      563 TTTCCGGCTCCCGC-AGAGAGGTGGCACCCCTATCAGGGGGGCTGACCCCATCTTCTTGC 721
Qy      326 aThrAlaLeuAla 330
Db      722 GACAAGCTCGCT 734

```

RESULT 5

```

BI860918

```

```

LOCUS

```

```

DEFINITION

```

```

5', mRNA sequence.

```

```

ACCESSION

```

```

VERSION

```

```

BM546826 1070 bp mRNA linear EST 20-FEB-2002

```

```

AGENCOURT 6491128 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:573557

```

```

BM546826

```

```

BM546826.1 GI:18780096

```



```

Db      654 TTCCAGTGTCAATTGACGCTCTGCCCTCAATGGGACCGTGCACCTCTCCCTGCCAGGAG 713
QY      161 LysGlnAsnThrValCysThrCysHisAlaGly-PhePheLeuArgGluAsnGluCysVa 180
Db      714 AAACAGACACCGTGGACCTGCCATGCAGGTTTCTTTCCTTAAGAGAAACGAGGTGT 773
QY      180 lSerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGl 200
Db      774 CTCCTGTACTACTGTAAAGADAAGCCTGGAGTGCACGAG-TTGTGCTACCCAGATTGA 832
QY      200 uAsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValLlePhePh 220
Db      833 GAATGTTAAGGCACTAGCACTACGACACGACGCTGTGCTCCCTCGTCAATTTCTT 892
QY      220 eGlyLeuCysLeuSerLeuPheIleGlyLeuMetTyrArgTyr 236
Db      893 TGTCTGTGCTTTATMCTCTCTCTTCATTTGTTTAAATGTATCGCTAC 941

RESULT 8
AL577008 975 bp mRNA linear EST 16-FEB-2001
LOCUS    AL577008 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0DI082YA01 5
DEFINITION
prime, mRNA sequence.
ACCESSION AL577008
VERSION   AL577008.1 GI:12939716
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 975)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..975
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI082YA01"
/clone_lib="LTI_NFL006.PL2"
/tissue_type="placenta"
/notes="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 231 a 258 c 259 g 221 t 6 others
ORIGIN
Alignment Scores:
Pred. No.: 3 63e-109 Length: 975
Score: 1245.50 Matches: 232
Percent Similarity: 96.27% Conservative: 0
Best Local Similarity: 96.27% Mismatches: 8
Query Match: 50.08% Indels: 4
DB: 9 Gaps: 0

US-09-899-422a-2 (1-455) x AL577008 (1-975)
QY      1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuVal 20
Db      256 ATGGGCTCTCCACCGCTGCTGCTGCTGCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
QY      21 GlyIleTyrProSerGlyValLleGlyLeuValProHisLeuGlyAspArgGluLysArg 40

```

```

Db      316 GGAATATACCCCTCAGGGGTATTGGACTGGTCCCTCACCTAGGACAGGAGAAAGA 375
QY      41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnSerIleCysCysThr 60
Db      376 GATAGTGTGTGTCCTCCCAAGAAATATATCCACCCCTCAAAATATTCGATTCTGCTACC 435
QY      61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
Db      436 AAGTGCCACAAAGAAACCTTACTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGAC 495
QY      81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db      496 TGCAGGAGTGTGTGCTGCTCCCTTCACCGCTTCAGAAACACACCTCAGACACTGCCTC 555
QY      101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db      556 AGCTGCTCCAAATGCCAAGGAATGGGTGAGTGGAGATCTCTTCTTCACAGTGGAC 615
QY      121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
Db      616 CGGGACACCGTGTGTGCTGCAGGAAGAACCTACCGGCATTATTGGAGTGAACCTT 675
QY      141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db      676 TTCAGTGTCTTCAATTGCAGCCTCTGCCTCAATGGGACCTGCACCTCTCCTGCGCAGG 735
QY      161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db      736 AAACAGAACACCTGTGCTGCCCTGCCATGCGATTTCTTCTTAAGAGAAACGAGTGTGTC 795
QY      181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeu-CysLeuProGlnIleGl 200
Db      796 TYCTGTAGTAACCTGTDAAGAAAGCCTGGAGTGCACGAAGTTGTGCTACCCAGATTGA 855
QY      200 uAsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValLlePhePh 220
Db      856 GAATGTTAAGGCACTGAGGACTCAGGCACCAAGTGTCTGCCCTGCTCATTTCTT 915
QY      220 eGlyLeuCysLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTyr 240
Db      916 TGTCTTTTGGCT-TTATCCCC-CTCTTCATTTGTTTAAATGATGCTGCTACCAASG-TGGAA 972
QY      240 s 240
Db      973 G 973

RESULT 9
LOCUS    BG180101
DEFINITION
602329676F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4431019 5',
mRNA sequence.
ACCESSION BG180101
VERSION   BG180101.1 GI:12686804
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 974)
NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10185 row: 9 column: 20

```

[illegible]


```

QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
DB 226 GGAATATACCCCTCAGGGTTATTTGGACTGGTCCCTCACCCTAGGGACAGGGAGAGAGA 285

QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAspSerIleCysCysThr 60
DB 286 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 345

QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
DB 346 AAGTCCCAACAAGGAACCTACTTGTACAAATGACTCTCCAGGCCCGGGCAGGATACGGAC 405

QY 81 CysArgGluCysLysSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
DB 406 TGCAGGGAGTGTGAGCGGGCTCTTCACCGCTTCAGAAACACCTCAGACACTGCCTC 465

QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
DB 466 AGCTGCTCCAAATGCCGAAGGAATGGTCAAGTGGAGATCTCTTCTGACACATGGAC 525

QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
DB 526 CGGGACACCGTGTGTGGCTGCAGGAAGAACCACTACAGCATATTGGAGTGAACACCTT 585

QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
DB 586 TTCCAGTGTCTCAATGGAGCCTCTGCCTCAATGGAGCGGTGCACCTCTCTCGCCAGGAG 645

QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
DB 646 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTCTTCTTAAGAGAAACAGTGTGTC 705

QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGln-IleG1 200
DB 706 TCCTGTAGTAAGTAAGAAAGCCTGGAGTGCAGGAAGTGTGCCTACCCACCATGNA 765

QY 200 uasnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIle-Phe- 219
DB 766 GAATGTTAAGGCACTGGAGCTCAGGCACCACTGCTGTGTGGCCCGGNCATTNTTCT 825

QY 220 PheGlyLeuCysLeuSerLeu---LeuPheIleGlyLeuMetTyrArgTyrGlnArg 238
DB 826 TTTGGCTTGCCTTTTATCCCTCCCTCCCTCCATTTGGTTAAATGGATCGTACCCACG 885

QY 239 ---TrpLysSerLysLeuTyr-SerIleValCys-GlyLysSerThrPro-----GluL 255
DB 886 GGGGGAATATCAAGCTCTACCTCCCTTGTGTGTGGGGGAAACCCACCCCTGGAAA 945

QY 255 ysGluGlyGluLeuGluGlyThrThrThrLysProLeuAlaProAsnProSerPheSerP 275
DB 946 AAGAAGGG-----GGGAAACCTTTGTG-AAGGAACCTTCC---TCCTC 983

QY 275 roThrPro 277 889 bp mRNA linear EST 01-AUG-2002
DB 984 CTAACCC 991

RESULT 11
AUI17362
LOCUS AUI17362 HEMBA1 Homo sapiens cDNA clone HEMBA1001229 5', mRNA
DEFINITION sequence.
ACCESSION AUI17362
VERSION AUI17362.1 GI:10932324
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 889)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cDNA project
TITLE

```

JOURNAL
COMMENT

Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute

FEATURES
source

Location/Qualifiers
1..889
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEMBA1001229"
/clone_lib="HEMBA1"
/tissue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/note="Vector: pME18SFL3"

BASE COUNT 167 a 301 c 249 g 166 t 6 others
ORIGIN

Alignment Scores:

Pred. No.: 1..98e-105 Length: 889
Score: 1206.00 Matches: 230
Percent Similarity: 98.71% Conservative: 0
Best Local Similarity: 98.71% Mismatches: 3
Query Match: 48.49% Indels: 1
DB: 9 Gaps: 0

US-09-899-422A-2 (1-455) x AUI17362 (1-889)

```

QY 223 CysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLysSerLys 242
DB 3 TCCTTTTATCCCTCTCTTCATTTGTTAAATGATACGCTACCAAGTGGAGTCAAG 62

QY 243 LeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeuGluGlyThr 262
DB 63 CTCCTACTCCATTTGTTGGAAATCGACACCTGAAAGAGGGGAGCTTGAAGNACT 122

QY 263 ThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThrProThr 282
DB 123 ACTACTAAGCCCTGGCCCCNAACCCAGCTTCAGTCCACCTCCAGCTTACCCACCC 182

QY 283 LeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThrProGly 302
DB 183 CTGGGCTTCAGTCCCGTGGCCAGTTCACCTTCACCTCCAGCTCCACCTATACCCCGT 242

QY 303 AspCysProAsnPheAlaAlaProArgGluValAlaProProTyrGlnGlyAlaAsp 322
DB 243 GACTGTCCCACTTTTGGGCTCCCGCAGAGAGTGGCACCACCTATCAGGGGCTGAC 302

QY 323 ProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLysTrpGlu 342
DB 303 CCCATCTTGGCAGACGCCCTCCGCTCCGACCCATCCCAACCCCTTCAGAGTGGAG 362

QY 343 AspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyrAlaVal 362
DB 363 GACAGGCCCAACAGCCACAGACCTAGACACTGATGACCCCGCAGCTGTACGCCGTG 422

QY 363 ValGluAsnValProProLeuArgTrpLysGluPheValArgLeuGlyLeuSerAsp 382
DB 423 GTGGAGAACGTGCCCGCTTGGCTTGGAGGAATTCGTGGCGGCTTAGGCTGAGCGAC 482

QY 383 HisGluIleAspArgLeuLeuGlnAsnGlyArgCysLeuArgGluAlaGlnTyrSer 402
DB 483 CACGAGATCATCGGCTGGAGCTGCAGAACGCGCGCTGCTGCGGAGCGCAATACAGC 542

QY 403 MetLeuAlaThrTrpArgArgThrProArgArgGluAlaThrLeuGluLeuGly 422
DB 543 ATGCTGGGACCTTGGAGCGCGCCACCGCCGCGGAGCGGCTGTGAGCTGTCTGGGA 602

```



```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4751536"
/clone_lib="NCI_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/notes="organ: skn; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: oligo dt.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      134 a    254 c    198 g    132 t
ORIGIN
Alignment Scores:
pred. No.:          1,44e-104          Length:          718
Score:             1195.50           Matches:         227
Percent Similarity: 95.38%           Conservative:     0
Best Local Similarity: 95.38%         Mismatches:      10
Query Match:       48.07%            Indels:          1
DB:                12                Gaps:            1

```

US-09-899-422A-2 (1-455) x BG680679 (1-718)

219	Qy	PhePheGlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArg	238
2	Db	TTCTTTGGTCTTTGGCTTTATTCCTCTCTTCATTTGGTTTAATGTATCGCTACCAACGG	61
239	Qy	TtpLysSerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGlu	258
62	Db	TGGAGTCCACAGCTCTACTCCATTGTTTGGGAATTCGACACCTGAAAAGAGGGGAG	121
259	Qy	LeuGluGlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGly	278
122	Db	CTTGAAGGAACACTACTAAGCCCTGGCCCCAACCAAGCTTCAGTCCCACTCCAGGC	181
279	Qy	PheThrProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThr	298
182	Db	TTACACCCCAACCTGGGCTTACGTCCCGTGGCCAGTTCCACCTTCACCTCCAGCTCCACC	241
299	Qy	TyrThrProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyr	318
242	Db	TATACCCCGGTGACTGTGCCAACCTTCGGGCTCCCGCAGAGAGGTGGCAACCACTAT	301
319	Qy	GlnGlyAlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeu	338
302	Db	CAGGGGGCTGACCCATCCTTCGCGACAGCCCTCGCTCCGACCCCAATCCCAATCCGCTT	361
339	Qy	GlnLysTrpGluAspSerAlaHisLysProGlnSerLeuLeuAspThrAspAspProAlaThr	358
362	Db	CAGAGTGGGAGACAGCGCCCAACAGCCACAGAGCTTAGACACTGATGACCCCGCGACG	421
359	Qy	LeuTyrAlaValAlaGluAsnValProProLeuLeuArgTrpLysGluPheValArgArgLeu	378
422	Db	CTGTAGCCGCTGGTGAGAACGTGCCCGCTTGGCTTGGAAAGGAATTCGTGGCGCGCTA	481
379	Qy	GlyLeuSerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGlu	398
482	Db	GGGCTCAGGACCCAGAGATCATCGGTGAGTGCAGAACGGGCGCTCCCTGCGCGAG	541
399	Qy	AlaGlnTyrSerMetLeuAlaThrTrpArgArgThrProArgArgGluAlaThrLeu	418
542	Db	GCSCAATACAGCATCTGGCGACCTGGAGCGCGCAGCCGCGCGCGAGGCCACGCTG	601
419	Qy	GluLeuLeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGlu	438
602	Db	GAGCTCTGGGACGGGTCTCGCGACATGGACCTGCTGGGCTGCCTGGAGGCACATCGA	661
439	Qy	GluAlaLeuCysGlyProAlaAlaLeuPro--ProAlaProSerLeuLeuArg	455
662	Db	GGAGGGCGTTTGGGGCCCCCGGACCTCCCGACCGCGGCGCCAGATCTTCTCAGA	715

RESULT 14
 BW742388

RESULT 14
BM742388

LOCUS	BM742388	669 bp	mrna	linear	EST 01-MAR-2002
DEFINITION	K-EST0015256 S6SNU620 Homo sapiens cDNA clone S6SNU620-5-C12 5', mRNA sequence.				
ACCESSION	BM742388				
VERSION	BM742388.1 GI:19063703				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Chordata; Metazoa; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.				
AUTHORS	1 (bases 1 to 669) Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.				
TITLE	21C Frontier Korean EST Project 2001				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 5 row: C column: 12 High quality sequence stop: 669.				
FEATURES	Location/Qualifiers				
source	1..669 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="S6SNU620-5-C12" /clone_lib="S6SNU620" /sex="F" /tissue_type="Ascites" /cell_type="Scattering floating" /cell_line="SNU-620" /lab_host="Top10p" /note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10p' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."				
BASE COUNT	128 a 239 c 193 g 109 t				
ORIGIN					

Alignment Scores:	
Pred. NO.:	1.79e-104
Score:	1194.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	48.01%
DB:	14
	Gaps: 0
	Indels: 0
	Mismatches: 0
	Conservative: 0
	Matches: 223
	Length: 669

US-09-899-422A-2 (1-455) x BM742388 (1-669)

Qy	230	IleGlyLeuMetTyrArgTyrGlnArgTrpLysSerLysLeuTyrSerIleValCysGly	249
Dδ	1	ATTGGTTTAATGTATCGCTACCAAGCGTGGAAGTCGAAGCTCTACTCCATGTGTTGGG	60

Qy	250	Lys	Ser	Thr	Pro	Glu	Lys	Glu	Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	269
Db	61	AAATCGGACAC	CTG	AAAAAGAGGGG	GAG	CTT	GAAGGA	AACTACT	ACT	TACT	TAA	GGCCCT	TGG	CCCA	120							

RESULT 14
BM742388

```

QY 270 AsnProSerPheSerProThrProGlyPheThrProThrLeuGlyPheSerProValPro 289
Db 121 AACCCAGCTTTCAGTCCACCTCCAGGCTTACCCGCCACCTCGGGCTTCAGTCCGCGCC 180
QY 290 SerSerThrPheSerSerSerThrThrProGlyAspCysProAsnPheAlaAla 309
Db 181 AGTTCCACCTTTCAGTCCACCTTACCCGCTTACCCGCTTACCCGCTTACCCGCTT 240
QY 310 ProArgArgGluValAlaProProTyrglnGlyAlaAspProIleLeuAlaThrAlaLeu 329
Db 241 CCCCGCAGAGAGTGGCACCACCTATCAGGGGCTGACCCCATCTTGGCAGACCCCTC 300
QY 330 AlaSerAspProIleProAsnProLeuGlnLysTrpGluAspSerAlaHisLysProGln 349
Db 301 GCCTCCGACCCCATCCCAACCCCTTCAAGAGTGGGAGGACAGCGCCCAAGCCACAG 360
QY 350 SerLeuAspThrAspAspProAlaThrLeuThrAlaValValGluAsnValProLeu 369
Db 361 AGCTAGACACTGATGACCCCGGACGCTGTACCGCTGTGGAGAACGTCGCCCGCTTG 420
QY 370 ArgTrpLysGluPheValArgLeuGlyLeuSerAspHisGluIleAspArgLeuGlu 389
Db 421 CGCTGGAAGGAATTCGTGGCGCTAGGGCTGAGCGCACGACGATCGATCGCTGGAG 480
QY 390 LeuGlnAsnGlyArgCysLeuArgGluAlaGlnTrpSerMetLeuAlaThrTrpArgArg 409
Db 481 CTGCAGAACGGGCGCTGCTCGCGGAGGCGCAATACAGCATGCTGGGCGACCTGGAGCGG 540
QY 410 ArgThrProAspArgGluAlaThrLeuGluLeuLeuGlyArgValLeuArgAspMetAsp 429
Db 541 CGCAGCGCGCGCGGAGGCGCACCTGAGCTGTGGACGCTGTGGCGGATCGATCGATG 600
QY 430 LeuLeuGlyCysLeuGluAspIleGluAlaLeuCysGlyProAlaAlaLeuProPro 449
Db 601 CTGCTGGGCTGCTGGAGGACATCGAGAGGCGCTTTGGGCGCGCGCGCTCCCGCC 660
QY 450 AlaProSer 452
Db 661 GCGCCCACT 669

RESULT 15
AL522989
LOCUS AL522989 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB009YPI4 5
DEFINITION prime, mRNA sequence.
ACCESSION AL522989
VERSION AL522989.1 GI:12786482
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .837
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DB009YPI4"
/clone_lib="LTI_NFL004_NBC2"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(GT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6

```

vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>*

BASE COUNT 199 a 231 c 229 g 177 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 4.97e-104 Length: 837
Score: 1191.00 Matches: 212
Percent Similarity: 99.53% Conservative: 0
Best Local Similarity: 99.53% Mismatches: 1
Query Match: 47.89% Indels: 0
DB: 9 Gaps: 0

US-09-899-422A-2 (1-455) x AL522989 (1-837)

```

QY 1 MetGlyLeuSerThrValProAspLeuLeuValLeuLeuGluLeuVal 20
Db 198 ATGGGCTCTCCACCGTGCCTGACCTGCTGCTGCACCTGGTCTCTGGAGCTGTGGT 257
QY 21 GlyIleThrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
Db 258 GGAATATACCCCTCAGGGGTATTGGACTGTGCTCCTCCTCCTAGGGGACAGGAGAGA 317
QY 41 AspSerValCysProGlnGlyLysThrIleHisProGlnAsnAsnSerIleCysCysThr 60
Db 318 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATAATTGATTTGCTGTACC 377
QY 61 LysCysHisLysGlyThrTyrrLeuTyrrAsnAspCysProGlyProGlyGlnAspThrAsp 80
Db 378 AAGTGCACAAAGGAACCTACTTGTACAATGACTGTCCAGGCCCGGGGAGGATACGGAC 437
QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db 438 TGCAGGAGGTGTGAGAGCGCTCCTTCCCGCTTCAGAAAACCAACCTCAGACACTGCCTC 497
QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db 498 AGCTGCTCCAAATGCCGAAAGGAATGGTCCAGTGGAGATCTCTTCTGCACAGTGGAC 557
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTrpArgHisTyrrTrpSerGluAsnLeu 140
Db 558 CGGACACCGCTGTGTGGCTGCAGGAAGAACAGTACCGGCATTTATTGGAGTGAACACTT 617
QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 618 TTCCAGTGTCTCAATTCAGCCTCTGCTCAATGGGACCTGTCACCTCTCTCTGCCAGGAG 677
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db 678 AAACAGAACACCGTGTGCACCTGCCATGCAGTCTTCTTTCTAAGAGAAAACAGTGTGTC 737
QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 738 TCCTGTAGTAACCTGAAGAAAAGCCTGGAGTGCAGGAAGTGTGCTTACCCACAGATTGAG 797
QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeu 213
Db 798 AATGTTAAGGGCACTGAGGACTCAGGCACCACTGCTGTG 836

```

Search completed: June 9, 2003, 02:39:40

Job time : 1573 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1366.4	99.9	2161	3	US-09-106-038A-1	Sequence 1, Appli
2	1366.4	99.9	2161	4	US-09-505-250-3	Sequence 3, Appli
3	1366.4	99.9	2175	1	US-08-321-668-1	Sequence 1, Appli
4	1366.4	99.9	2175	1	US-08-837-941-1	Sequence 1, Appli
5	1366.4	99.9	2175	1	US-08-126-016-1	Sequence 1, Appli
6	1366.4	99.9	2175	4	US-08-054-970-1	Sequence 1, Appli
7	1360	99.4	2062	1	US-08-050-319B-24	Sequence 24, Appli
8	1360	99.4	2062	2	US-08-465-982-24	Sequence 24, Appli
9	690.4	50.5	1956	2	US-08-762-308-10	Sequence 10, Appli
10	685.4	50.1	2440	4	US-09-513-007-1	Sequence 1, Appli
11	632.8	46.3	6896	2	US-08-627-151A-6	Sequence 6, Appli
12	632.4	46.2	6889	1	US-08-286-740-2	Sequence 2, Appli
13	632.4	46.2	6889	5	PCM-US95-09576-2	Sequence 2, Appli
14	593.6	43.4	600	1	US-08-050-319B-47	Sequence 47, Appli
15	593.6	43.4	600	2	US-08-465-982-47	Sequence 47, Appli
16	515.4	37.7	1478	4	US-09-149-922-6	Sequence 6, Appli
17	514	37.6	1301	4	US-08-804-166-7	Sequence 7, Appli
18	514	37.6	1301	4	US-08-910-991-7	Sequence 7, Appli
19	506	37.0	1147	4	US-08-804-166-5	Sequence 5, Appli
20	506	37.0	1147	4	US-08-910-991-5	Sequence 5, Appli
21	501.4	36.7	504	1	US-08-050-319B-56	Sequence 56, Appli
22	501.4	36.7	504	2	US-08-465-982-56	Sequence 56, Appli
23	499.4	36.5	501	1	US-08-050-319B-1	Sequence 1, Appli
24	499.4	36.5	501	2	US-08-465-982-1	Sequence 1, Appli
25	483	35.3	483	4	US-09-326-394-1	Sequence 1, Appli
26	424.4	31.0	1049	4	US-08-804-166-1	Sequence 1, Appli
27	424.4	31.0	1049	4	US-08-910-991-1	Sequence 1, Appli

Db 316 GGAATATATACCCCTCAGGGGTTATTGGACTGGTCCCTCACCTAGGGAGCAGGAGAGAGA 375
QY 121 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGCTGTACC 180
Db 376 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGCTGTACC 435
QY 181 AGTGCCCAAAAGAACCTTACTTGTACAAATGACTGTCCAGGCGGGGAGGATACGGAC 240
Db 436 AAGTGCCCAAAAGAACCTTACTTGTACAAATGACTGTCCAGGCGGGGAGGATACGGAC 495
QY 241 TGCAGGGAGTGTGAGAGCGGTCTCTTACCGCTTCAGAAACCAACCTCAGACACTGCCCTC 300
Db 496 TGCAGGGAGTGTGAGAGCGGTCTCTTACCGCTTCAGAAACCAACCTCAGACACTGCCCTC 555
QY 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTCCAGTGGAGATCTCTTTGACACAGTGAC 360
Db 556 AGCTGCTCCAAATGCCGAAAGAAATGGGTCCAGTGGAGATCTCTTTGACACAGTGAC 615
QY 361 CGGGACACCGTGTGGTGTGAGGAAACCAACCTACCGGCAATTTATGGAGTGAACACCTT 420
Db 616 CGGGACACCGTGTGGTGTGAGGAAACCAACCTACCGGCAATTTATGGAGTGAACACCTT 675
QY 421 TTCCAGTGTCAATTTGAGCGCTCTGCTCAATGGGACCGTGCACCTCTCTGCGAGAG 480
Db 676 TTCCAGTGTCAATTTGAGCGCTCTGCTCAATGGGACCGTGCACCTCTCTGCGAGAG 735
QY 481 AAACAGAACCGGTGTGCACCTGCCATGCGAGTGTCTTTTAAAGAGAAACAGTGTGTC 540
Db 736 AAACAGAACCGGTGTGCACCTGCCATGCGAGTGTCTTTTAAAGAGAAACAGTGTGTC 795
QY 541 TCCTGTACTAATTAAGAAAGCTGTGAGTGCAGAGTTGTGGCTACCCAGATTGAG 600
Db 796 TCCTGTACTAATTAAGAAAGCTGTGAGTGCAGAGTTGTGGCTACCCAGATTGAG 855
QY 601 AATGTTAAGGGCACTGAGGACTCAGGCACCAAGTGTGTTGCCCTGCTCATTTTCCTT 660
Db 856 AATGTTAAGGGCACTGAGGACTCAGGCACCAAGTGTGTTGCCCTGCTCATTTTCCTT 915
QY 661 GGTCTTTGCCCTTATCCCTCTCTTCAATGTTGTTAAATGATCGCTACCAACGGTGAAG 720
Db 916 GGTCTTTGCCCTTATCCCTCTCTTCAATGTTGTTAAATGATCGCTACCAACGGTGAAG 975
QY 721 TCCAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGA 780
Db 976 TCCAGCTCTACTCCATTTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGA 1035
QY 781 GGAATCTACTAAGCCCTCGCCCAACCAAGCTTCAGTCCACCTCCAGGCTTACC 840
Db 1036 GGAATCTACTAAGCCCTCGCCCAACCAAGCTTCAGTCCACCTCCAGGCTTACC 1095
QY 841 CCCACCTGGGCTTACGTCCCGTGGCCAGTTCCACCTTACCTCCAGCTCCACCTATACC 900
Db 1096 CCCACCTGGGCTTACGTCCCGTGGCCAGTTCCACCTTACCTCCAGCTCCACCTATACC 1155
QY 901 CCCGTGACTCTCCCAACTTTGCGGCTCCCGCAGAGAGTGGCACACCTATCAGGGG 960
Db 1156 CCCGTGACTCTCCCAACTTTGCGGCTCCCGCAGAGAGTGGCACACCTATCAGGGG 1215
QY 961 GCTCACCCCTCTTGGCACAGCCCTCGCTCCGACCCCACTCCCAACCCCTTCCAGAG 1020
Db 1216 GCTCACCCCTCTTGGCACAGCCCTCGCTCCGACCCCACTCCCAACCCCTTCCAGAG 1275
QY 1021 TGGAGGACAGCGGCCCAAGCCACAGACCTAGACACTGATGACCCCGCAGCGTGPAC 1080
Db 1276 TGGAGGACAGCGGCCCAAGCCACAGACCTAGACACTGATGACCCCGCAGCGTGPAC 1335
QY 1081 GCGTGTGGAGACGTGCCCTTGGCTGGAGGAAATTCGTGGCGCGCTAGGCGTG 1140
Db 1336 GCGTGTGGAGACGTGCCCTTGGCTGGAGGAAATTCGTGGCGCGCTAGGCGTG 1395
QY 1141 AGCGACACAGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCTCGCGGAGCGCAA 1200
Db 1396 AGCGACACAGAGATCGATCGGCTGGAGCTGCAGAACGGGCGCTGCTCGCGGAGCGCAA 1455

QY 1201 TACAGCATGCTGGGACCTGGAGGGGGCCACGGCGGCGGAGCCACGCTGGAGCTG 1260
Db 1456 TACAGCATGCTGGGACCTGGAGGGGGCCACGGCGGCGGAGCCACGCTGGAGCTG 1515
QY 1261 CTGGACCGGTGCTCCGCGACATGACCTGTGTGGCTGCCCTGGAGGACATCAGAGAGCG 1320
Db 1516 CTGGACCGGTGCTCCGCGACATGACCTGTGTGGCTGCCCTGGAGGACATCAGAGAGCG 1575
QY 1321 CTTTGGCGCGCGCGCGCTCCCGCGCGCGCGCTCTTCAGATGA 1368
Db 1576 CTTTGGCGCGCGCGCGCTCCCGCGCGCGCGCTCTTCAGATGA 1623

RESULT 2

US-09-505-250-3
; Sequence 3, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Kao, Peter
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2161
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (256)...(1623)
US-09-505-250-3

Query Match 99.9%; Score 1366.4; DB 4; Length 2161;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCTCTCCACCGTGCCTGACCTGCTGTGCTGCACCTGGTGTCTCTGGAGCTGTGGTG 60
Db 256 ATGGGCTCTCCACCGTGCCTGACCTGCTGTGCGCTGGTGTCTCTGGAGCTGTGGTG 315
QY 61 GGAATATACCCCTCAGGGGTTATTGGACTGTGCTCCTACCTAGGGGACAGGAGAGA 120
Db 316 GGAATATACCCCTCAGGGGTTATTGGACTGTGCTCCTACCTAGGGGACAGGAGAGA 375
QY 121 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGCTGTACC 180
Db 376 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGCTGTACC 435
QY 181 AAGTGCCCAAAAGAACCTTACTTGTACAAATGACTGTCCAGGCGGGGAGGATACGGAC 240
Db 436 AAGTGCCCAAAAGAACCTTACTTGTACAAATGACTGTCCAGGCGGGGAGGATACGGAC 495
QY 241 TGCAGGGAGTGTGAGAGCGGTCTCTTACCGCTTCAGAAACCAACCTCAGACACTGCCCTC 300
Db 496 TGCAGGGAGTGTGAGAGCGGTCTCTTACCGCTTCAGAAACCAACCTCAGACACTGCCCTC 555
QY 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTCCAGTGGAGATCTCTTTGACACAGTGAC 360
Db 556 AGCTGCTCCAAATGCCGAAAGAAATGGGTCCAGTGGAGATCTCTTTGACACAGTGAC 615
QY 361 CGGGACACCGTGTGGTGTGAGGAAACCAACCTACCGGCAATTTATGGAGTGAACACCTT 420
Db 616 CGGGACACCGTGTGGTGTGAGGAAACCAACCTACCGGCAATTTATGGAGTGAACACCTT 675
QY 421 TTCCAGTGTCTCAATTTGAGCGCTCTGCTCAATGGGACCGTGCACCTCTCTGCGAGAG 480
Db 676 TTCCAGTGTCTCAATTTGAGCGCTCTGCTCAATGGGACCGTGCACCTCTCTGCGAGAG 735

```
QY 481 AAACAGAACACCGCTGCGACCTGCCATGAGAGTTCCTTTCTAAGAGAAACAGAGTGTG 540
Db 736 AAACAGAACACCGCTGCGACCTGCCATGAGAGTTCCTTTCTAAGAGAAACAGAGTGTG 795
QY 541 TCCTGTAGTAACCTGAAGAAACCTGGAGTGCACCAAGTGTGCTACCCAGATGAG 600
Db 796 TCCTGTAGTAACCTGAAGAAACCTGGAGTGCACCAAGTGTGCTACCCAGATGAG 855
QY 601 AATGTTAAGGGCACTGAGGACTCAGGCACACAGTGTGCTGTCCTGCTGCTGCTGCTGCT 660
Db 856 AATGTTAAGGGCACTGAGGACTCAGGCACACAGTGTGCTGTCCTGCTGCTGCTGCTGCT 915
QY 661 GGTCTTTGCTTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 916 GGTCTTTGCTTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 975
QY 721 TCCAACTCTACCTCCATGTTTCTGGAAATGACACACTGAAAGAGGGGAGCTTGA 780
Db 976 TCCAACTCTACCTCCATGTTTCTGGAAATGACACACTGAAAGAGGGGAGCTTGA 1035
QY 781 GGAATCTACTAAGCCCTGCGCCCAACCCCAAGCTTCAGTCCCACTCCAGCTTCACC 840
Db 1036 GGAATCTACTAAGCCCTGCGCCCAACCCCAAGCTTCAGTCCCACTCCAGCTTCACC 1095
QY 841 CCCACCTGGCTTCAGTCCGCTGCGCCCAAGCTTCACCTTCACCTTCACCTTCACCT 900
Db 1096 CCCACCTGGCTTCAGTCCGCTGCGCCCAAGCTTCACCTTCACCTTCACCTTCACCT 1155
QY 901 CCCGCTGACTGCTCCAACTTTGGGCTCCCGCAGAGAGTGCACACCCCTATCAGGG 960
Db 1156 CCCGCTGACTGCTCCAACTTTGGGCTCCCGCAGAGAGTGCACACCCCTATCAGGG 1215
QY 961 GCTGACCCCTCTCTGCGACAGCCCTGCGCTCGGACCCCTCCCAACCCCTTCAGAG 1020
Db 1216 GCTGACCCCTCTCTGCGACAGCCCTGCGCTCGGACCCCTCCCAACCCCTTCAGAG 1275
QY 1021 TGGAGGACAGCCGACACAGCCACAGAGCTTACCTTCACCTTCACCTTCACCTTCAC 1080
Db 1276 TGGAGGACAGCCGACACAGCCACAGAGCTTACCTTCACCTTCACCTTCACCTTCAC 1335
QY 1081 GCGCTGTGAGAACGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 1140
Db 1336 GCGCTGTGAGAACGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 1395
QY 1141 AGCGACACAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db 1396 AGCGACACAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1455
QY 1201 TACAGCATGCTGGAGCTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1260
Db 1456 TACAGCATGCTGGAGCTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1515
QY 1261 CTGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db 1516 CTGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1575
QY 1321 CTTTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
Db 1576 CTTTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1623
```

RESULT 3

```
US-08-321-668-1
; Sequence 1, Application us/08321668
; Patent No. 5665859
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARFOLOMEY, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,668
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107268
; FILING DATE: 12-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2175 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 256..1620
; US-08-321-668-1
```

```
Query Match 99.9%; Score 1366.4; DB 1; Length 2175;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCTCTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Db 256 ATGGGCTCTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315
QY 61 GGAATATACCCCTCAGGGGTATTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 316 GGAATATACCCCTCAGGGGTATTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 375
QY 121 GATAGTGTGTGCTCCCAAGGAAATATATCCACCTCAAAATATATTCGATTGCTGTACC 180
Db 376 GATAGTGTGTGCTCCCAAGGAAATATATCCACCTCAAAATATATTCGATTGCTGTACC 435
QY 181 AAGTGCACAAAGAAACCTACTTGTACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 436 AAGTGCACAAAGAAACCTACTTGTACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 495
QY 241 TGCAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAACACCTCAGACACTGCCTC 300
Db 496 TGCAGGAGTGTGAGAGCGGCTCCTTCACCGCTTCAGAAACACCTCAGACACTGCCTC 555
QY 301 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGATCTCTTCTTCCACAGTGGAC 360
Db 556 AGCTGCTCCAAATGCCGAAAGAAATGGGTGAGATCTCTTCTTCCACAGTGGAC 615
QY 361 CGGACACACCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 616 CGGACACACCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
QY 421 TTCAGTGTCTCAATTGACGCTCTGCTCAATGGGACCTGCTGCTGCTGCTGCTGCTGCTGCT 480
|||||
```


Qy	301	AGCTGCTCCAAATCCCGAAAGGAATGGGTGTCAGGTGGAGATCTCTTCTTGACAGTGGAC	360
Db	556	AGCTGCTCCAAATCCCGAAAGGAATGGGTGTCAGGTGGAGATCTCTTCTTGACAGTGGAC	615
Qy	361	CGGACACCGGTGTGTGCTGCAGGAACAACAGTACCGGCATTTATGGAGTGAACAACCTT	420
Db	616	CGGACACCGGTGTGTGCTGCAGGAACAACAGTACCGGCATTTATGGAGTGAACAACCTT	675
Qy	421	TTCCAGTGTTCAAATTGACGCTCTGCCTCAATGGGACCGTGCACCTCTCTCTGCCAGGAG	480
Db	676	TTCCAGTGTTCAAATTGACGCTCTGCCTCAATGGGACCGTGCACCTCTCTCTGCCAGGAG	735
Qy	481	AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTAAGAGAAAACGAGTGTCTC	540
Db	736	AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTAAGAGAAAACGAGTGTCTC	795
Qy	541	TCCTGTAGTAACTGTAAAGAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCACAGATTGAG	600
Db	796	TCCTGTAGTAACTGTAAAGAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCACAGATTGAG	855
Qy	601	AATGTTAAGGCACTGAGGACTCAGGCACACAGTGTCTGTGGCCCTGGTCAATTTCTTT	660
Db	856	AATGTTAAGGCACTGAGGACTCAGGCACACAGTGTCTGTGGCCCTGGTCAATTTCTTT	915
Qy	661	GGTCTTTGGCTTTTATCCCTCCTCTTCATTTGTTTAAATGTATGCTACCAACGGTGGAG	720
Db	916	GGTCTTTGGCTTTTATCCCTCCTCTTCATTTGTTTAAATGTATGCTACCAACGGTGGAG	975
Qy	721	TCCAAGCTCTACTCCATTTGTTTGGGAAATCGACACCTGAAAAGAGGGGAGCTTGAA	780
Db	976	TCCAAGCTCTACTCCATTTGTTTGGGAAATCGACACCTGAAAAGAGGGGAGCTTGAA	1035
Qy	781	GGAACTACTTAAGCCCTTGGCCCCAAACCCAGCTTCAGTCCCACTCCAGGCTTCACC	840
Db	1036	GGAACTACTTAAGCCCTTGGCCCCAAACCCAGCTTCAGTCCCACTCCAGGCTTCACC	1095
Qy	841	CCCACCTGGGCTTCAGTCCCGTGCCAGTTTCCACCTTCACCTCCAGCTCCACCTATACC	900
Db	1096	CCCACCTGGGCTTCAGTCCCGTGCCAGTTTCCACCTTCACCTCCAGCTCCACCTATACC	1155
Qy	901	CCCGGTGACTGTCCCAACTTTGGGGCTCCCGGCAGAGAGTGGACACACCTATCAGGGG	960
Db	1156	CCCGGTGACTGTCCCAACTTTGGGGCTCCCGGCAGAGAGTGGACACACCTATCAGGGG	1215
Qy	961	GCTGACCCCATCTCTGGACAGCCCTCGCCTCCGACCCCATCCCAACCCCTTCAGAAG	1020
Db	1216	GCTGACCCCATCTCTGGACAGCCCTCGCCTCCGACCCCATCCCAACCCCTTCAGAAG	1275
Qy	1021	TGGAGAGACAGCGCCCAAGACCAAGAGCCTTAGACACTGATGACCCCGGAGCGCTGTAC	1080
Db	1276	TGGAGAGACAGCGCCCAAGACCAAGAGCCTTAGACACTGATGACCCCGGAGCGCTGTAC	1335
Qy	1081	GGCTGGTGGAGAACGTGCCCGCTTCCGCTGGAAGGAATTCGTGGCGGCCCTAGGGCTG	1140
Db	1336	GGCTGGTGGAGAACGTGCCCGCTTCCGCTGGAAGGAATTCGTGGCGGCCCTAGGGCTG	1395
Qy	1141	AGCGACACAGATTCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAA	1200
Db	1396	AGCGACACAGATTCGATCGGCTGGAGCTGCAGAACGGGCGCTGCCTGCGCGAGGCGCAA	1455
Qy	1201	TACAGCATGTGGGACCTGGAGGGCGGCACGCGCGGGCGGAGGCCACCGTGGAGCTG	1260
Db	1456	TACAGCATGTGGGACCTGGAGGGCGGCACGCGCGGGCGGAGGCCACCGTGGAGCTG	1515
Qy	1261	CTGGGAGCGCTGCTCCGCGACATGGACCTGCTGGGCTGCTTGGAGGACATCGAGGAGGGC	1320
Db	1516	CTGGGAGCGCTGCTCCGCGACATGGACCTGCTGGGCTGCTTGGAGGACATCGAGGAGGGC	1575
Qy	1321	CTTTGGGGCCCCGGCCCTCCCGCGCGCGCCCGAGTCTTCTCAGATGA	1368
Db	1576	CTTTGGGGCCCCGGCCCTCCCGCGCGCGCCCGAGTCTTCTCAGATGA	1623

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999

```

Query Match	99.9%	Score 1366.4	DB 4	Length 2175				
Best Local Similarity	99.9%	Pred. No. 0						
Matches 1367	Conservative	0	Mismatches	1	Indels	0	Gaps	0
Qy	1	ATGGGGCTCTCCACCGTGCCCTGACCTGACCTGCTGCTGCCACTGGTGTCTCTCTGAGAGCTGTTGGTG	60					
Db	256	ATGGGGCTCTCCACCGTGCTGACCTGACCTGCTGCTGCCGCTGGTGTCTCTCTGAGAGCTGTTGGTG	315					
Qy	61	GGAATATACCCCTCAGGGGTTATTGGACGTGGTCCCTCACCTAGGGGACACGGGAGAAGAGA	120					
Db	316	GGAATATACCCCTCAGGGGTTATTGGACGTGGTCCCTCACCTAGGGGACACGGGAGAAGAGA	375					
Qy	121	GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCCTCAAAATAATTCGATTTGCTGTACC	180					
Db	376	GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCCTCAAAATAATTCGATTTGCTGTACC	435					
Qy	181	AACTGCCACAAAGGAACCTACTTGTACATGACTGTCCAGGCCCGGGGGACAGNATCGGAC	240					
Db	436	AACTGCCACAAAGGAACCTACTTGTACATGACTGTCCAGGCCCGGGGGACAGNATCGGAC	495					
Qy	241	TGCAGGGAGTGTGAGAGCGGCTCTCTTCACCGCTTCAGAAAAACCACTTCAGACACTGCCCTC	300					
Db	496	TGCAGGGAGTGTGAGAGCGGCTCTCTTCACCGCTTCAGAAAAACCACTTCAGACACTGCCCTC	555					
Qy	301	AGCTGTCTCCAAATGCCGAAGGAAATGGGTTCAGGTGGAGATCTCTTTCTTGCACAGTGGAC	360					
Db	556	AGCTGTCTCCAAATGCCGAAGGAAATGGGTTCAGGTGGAGATCTCTTTCTTGCACAGTGGAC	615					

QY 421 TTCCAGTGTTCATTAATTCAGCCTCTGCCTCAATGGAGCGTGACCTCTCTCTCCAGGAG 480
DB 575 TTCCAGTGTTCATTAATTCAGCCTCTGCCTCAATGGAGCGTGACCTCTCTCTCCAGGAG 634
QY 481 AAACAGACACCGTGTGACCTGCCATGCAGTGTCTTCTTAAGAGAAACAGTGTGTC 540
DB 635 AAACAGACACCGTGTGACCTGCCATGCAGTGTCTTCTTAAGAGAAACAGTGTGTC 694
QY 541 TCCTGTAGTAAGTAAAGAAAGCCTGGAGTGCAGAAAGTGTGTGCTACCCAGATTGAG 600
DB 695 TCCTGTAGTAAGTAAAGAAAGCCTGGAGTGCAGAAAGTGTGTGCTACCCAGATTGAG 754
QY 601 AATGTTAAGGACCTGAGGACCTAGCAGCCACAGTGTGTGCTGCTGCTGCTGCTGCTGCT 660
DB 755 AATGTTAAGGACCTGAGGACCTAGCAGCCACAGTGTGTGCTGCTGCTGCTGCTGCTGCT 814
QY 661 GGTCTTTGCTTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
DB 815 GGTCTTTGCTTTTATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 874
QY 721 TCCAAAGCTCTACTCATTTGTTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 780
DB 875 TCCAAAGCTCTACTCATTTGTTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 934
QY 781 GGAAGTCTACTAAGCCCTGCGCCCAACCAAGCTTCAAGTGTGCTGCTGCTGCTGCTGCT 840
DB 935 GGAAGTCTACTAAGCCCTGCGCCCAACCAAGCTTCAAGTGTGCTGCTGCTGCTGCTGCT 994
QY 841 CCCACCTGCGCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 995 CCCACCTGCGCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054
QY 901 CCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 1055 CCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1114
QY 961 GGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 1115 GGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1174
QY 1021 TGGGAGGACGCGCCCAAGCAGACGCTGAGACCTGATGACCTGACCTGCGGCGGCTGAC 1080
DB 1175 TGGGAGGACGCGCCCAAGCAGACGCTGAGACCTGATGACCTGACCTGCGGCGGCTGAC 1234
QY 1081 GCGGTGTGGAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 1235 GCGGTGTGGAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1294
QY 1141 AGCGACACGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 1295 AGCGACACGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1354
QY 1201 TACAGCATGCTGCGGACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1260
DB 1355 TACAGCATGCTGCGGACCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1414
QY 1261 CTGGACCGGCTGCTGCGGACATGAGACCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1415 CTGGACCGGCTGCTGCGGACATGAGACCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1474
QY 1321 CTTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1368
DB 1475 CTTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1522

RESULT 8

US-08-465-982-24
; Sequence 24, Application US/08465982
; Patent No. 5863786
; GENERAL INFORMATION:
; APPLICANT: M. Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M. Brennan

; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,982
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319
; FILING DATE: 10-May-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Robert L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..1519
US-08-465-982-24

Query Match 99.4%; Score 1360; DB 2; Length 2062;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1363; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGGCTCTCCACCGTGCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
DB 155 ATGGGCTCTCCACCGTGCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 214
QY 61 GGAATATACCCCTCAGGCGTTCATGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 215 GGAATATACCCCTCAGGCGTTCATGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 274
QY 121 GATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 275 GATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 334
QY 181 AAGTGCCCAAGAAACCTACTTGTACAAATGATATCCACCTCAAAATATTCGATTTGCTGTAC 240
DB 335 AAGTGCCCAAGAAACCTACTTGTACAAATGATATCCACCTCAAAATATTCGATTTGCTGTAC 394
QY 241 TGCAGGAGTGTGAGAGCGGCTCCTTACCCGCTTACAGAAACCACTGAGAGTGTGCTGCTGCTGCT 300
DB 395 TGCAGGAGTGTGAGAGCGGCTCCTTACCCGCTTACAGAAACCACTGAGAGTGTGCTGCTGCTGCT 454
QY 301 AGCTGCTCAAAATGCGGAAAGAAATGGGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 455 AGCTGCTCAAAATGCGGAAAGAAATGGGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514
QY 361 CGGACACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 515 CGGACACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 574

QY 421 TTCCAGTGTTCATTCAGGCTCTGCTCAATGGGACCGTGCACCTCTCCCTGCCAGGAG 480
 Db 575 TTCCAGTGTTCATTCAGGCTCTGCTCAATGGGACCGTGCACCTCTCCCTGCCAGGAG 634
 QY 481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTCTTTCTTAAGAGAAACAGGTGTCTC 540
 Db 635 AAACAGAACACCGTGTGCACCTGCCATGCAGGTCTTTCTTAAGAGAAACAGGTGTCTC 594
 QY 541 TCCGTGTAGTAACTGAAGAAAGCCCTGGAGTGCAGAAAGTTGTGCTATCCCGAGATTGAG 600
 Db 695 TCCGTGTAGTAACTGAAGAAAGCCCTGGAGTGCAGAAAGTTGTGCTATCCCGAGATTGAG 754
 QY 601 AATGTTAAGGACCTGAGGACCTCAGGACCCAGAGCTGTGCTGCTGCTGCTGCTGCTGCT 560
 Db 755 AATGTTAAGGACCTGAGGACCTCAGGACCCAGAGCTGTGCTGCTGCTGCTGCTGCTGCT 814
 QY 661 GGTCTTTGCTGCTTTATCCCTCTCTCTTCAATGCTTTTAAATGCTATGCTTACCAAGCTGGAAG 720
 Db 815 GGTCTTTGCTGCTTTATCCCTCTCTCTTCAATGCTTTTAAATGCTATGCTTACCAAGCTGGAAG 874
 QY 721 TCCAGCTCTACTCCATGTTTGTGGGAAATCCACACCTGAAAGAGGGGAGCTTGAA 780
 Db 875 TCCAGCTCTACTCCATGTTTGTGGGAAATCCACACCTGAAAGAGGGGAGCTTGAA 934
 QY 781 GGAATCTACTAAGCCCTGSCCCCAACCCAGCTTCAGTCCGACTCCAGCTTCAC 840
 Db 935 GGAATCTACTAAGCCCTGSCCCCAACCCAGCTTCAGTCCGACTCCAGCTTCAC 994
 QY 841 CCCACCTGGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 Db 995 CCCACCTGGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054
 QY 901 CCGGTGTACTGCCAATTTTGGGCTCCCGCAGAGAGTGGGACCCATCAGGGG 960
 Db 1055 CCGGTGTACTGCCAATTTTGGGCTCCCGCAGAGAGTGGGACCCATCAGGGG 1114
 QY 961 GGTGACCCCATCTTGGGACAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 Db 1115 GGTGACCCCATCTTGGGACAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1174
 QY 1021 TGGGAGGACAGGCGCCACAGCCCTAGACACTGATGACCCCGGCGAGCTGTATC 1080
 Db 1175 TGGGAGGACAGTGCACAGCCACAGAGCCCTAGACACTGATGACCCCGGCGAGCTGTATC 1234
 QY 1081 GCGGTGGTGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 Db 1235 GCGGTGGTGAAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1294
 QY 1141 AGCGACACGAGATCGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 Db 1295 AGCGACACGAGATCGATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1354
 QY 1201 TACAGATGCTGGGACCTGGAGGCGGCGACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1260
 Db 1355 TACAGATGCTGGGACCTGGAGGCGGCGACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1414
 QY 1261 CTGGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 Db 1415 CTGGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1474
 QY 1321 CTTTGGGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1368
 Db 1475 CTTTGGGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1522

RESULT 9

US-08-762-308-10

; Sequence 10, Application US/08762308

; Patent No. 5925548

; GENERAL INFORMATION:

; APPLICANT: Beutler, Bruce A.

; APPLICANT: Bazzoni, Flavia M.

; TITLE OF INVENTION: MODIFIED RECEPTORS THAT CONTINUOUSLY

; TITLE OF INVENTION: SIGNAL
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77210-4433
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/762,308
 ; FILING DATE: 09-DEC-1996
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/224,593
 ; FILING DATE: 05-APR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kitchell, Barbara S.
 ; REGISTRATION NUMBER: 33,928
 ; REFERENCE/DOCKET NUMBER: UTSD:335--1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 418-3000
 ; TELEFAX: 474-7577
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1956 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-762-308-10

Query Match 50.5%; Score 690.4; DB 2; Length 1956;

Best Local Similarity 72.2%; Pred. No. 3.3e-156;

Matches 975; Conservative 0; Mismatches 351; Indels 24; Gaps 5;

QY 1 ATGGGCTCTCCACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
 Db 96 ATGGGCTCTCCACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 155
 QY 61 GGAATATACCCCTCAGGGGTATTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 Db 156 GGGATATACCTCATCAGGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 215
 QY 121 GATAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 Db 216 GATAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 275
 QY 181 AAGTGCCACAAAGGAACCTACTTGTACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 Db 276 AAGTGCCACAAAGGAACCTACTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 335
 QY 241 TGCAGGAGTGTGAGAGCGGCTCTTTCACGCTTTCAGAAACCAACCTCAGACACTGCTGCTGCTGCT 300
 Db 336 TGCAGGAGTGTGAGAAAGGCGACCTTTACGGCTTCCAGAAATTAACCTCAGGAGTGTGCTGCTGCT 395
 QY 301 AGCTGCTCCAAATGCCGAAGAAATGGGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 Db 396 AGTTGCAAGACATGCTCGGAAAGAAATGTCCAGGTGGAGATCTCTCTCTCCCAAGCTGAC 455
 QY 361 CGGGACACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Db 456 AAGGACACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 515
 QY 421 TTCCAGTGTTCATTCAGGCTCTGCTCAATGGGACCGTGCACCTCTCTCTGCCAGGAG 480
 Db 516 TTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 575
 QY 481 AAACAGAACACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

Db 576 ACTCAGAACCGTGTGAACCTGCATCAGGGTCTTTCTGAGAGAAAGTGAAGTGCCTC 635
Qy 541 TCCTGTACTAATTAAGAAAGCGTGGAGTGCAGAAAGTGTGCTA---CCCGAGATT 597
Db 636 CTTGACACCACTGCAAGAAAGAGAGAGTGTATGAAGTGTGCTACCTCCTCCGCTT 695
Qy 598 GAGAAATTAAGGCACTGAGGACTCAGGACCAAGCTGCTGTGCTGCTGCTGCTGCTGCT 657
Db 696 GCAATGTACAAACCCCGAGGACTCAGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 755
Qy 658 TTTGGTCTTGGCTTTATCCCTCCTCTTCATGTTGTTAAATGATATGATATGATATGAT 717
Db 756 CTAGTCTTGGCTTCTATCTCTTATCTTCATGTTGTTAAATGATATGATATGATATGAT 815
Qy 718 AAGTCCAAAGCTCTACTCCTATGTTGTTGGAAATGACACCTGAAAGAGAGGGAGCTT 777
Db 816 AGGCCGGAAGTCTACTCCTATGTTAGGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 875
Qy 778 GAAGAACTACTACTAAGCCCTGCGCCCAACCAAGCTTCAAGTCCACCTCCAGGCTTC 837
Db 876 GGAAGCCCTTAAGT-----CCAGCCCTCCCGAGCTTCAAGCTTCAAGCTTCAAGCT 929
Qy 838 ACCCCACCTTGGGCTCAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
Db 930 AACCCCACTCTGGGCTTCAAGCACCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 989
Qy 898 ACCCCCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 948
Db 990 AGCCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1049
Qy 949 CCCTATCAGGGGCTGACCCCACTGCTGCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1008
Db 1050 ACC---CAGGGAGCTGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1106
Qy 1009 CCCCTCAGAGTGGGAGCAGCGCCCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1068
Db 1107 TCTGTTCAAGTGGGAAGCTCGCCCACT---CCGCAAGCTGCTGCTGCTGCTGCTGCTG 1163
Qy 1069 CGGAGCTGTACCGGCTGGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1128
Db 1164 CGGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1223
Qy 1129 CGCTGAGGCTGAGGACCAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1188
Db 1224 TTCATGGGCTGAGCGACAGAGATCGAGAGGCTGAGAGTGCAGAGCGGCTGCTGCTG 1283
Qy 1189 CGGAGGCGCAATACAGATGCTGCGACCTGAGGAGGCGGCGGCGGCGGCGGCGGCGG 1248
Db 1284 CGGAGGCTCAGTACAGATGCTGGAAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1343
Qy 1249 ACCTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1308
Db 1344 ACCTGGAAGTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1403
Qy 1309 ATCAGGAGGCGCTTTGGGCGCCCGCGCGCC 1338
Db 1404 ATCTCGAGGCTGAGAAATCCGCGCC 1433

RESULT 10

US-09-513-007-1
; Sequence 1, Application US/09513007
; Patent No. 6406907
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehrl, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Wnangi, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBER: US/09/513.007

; CURRENT FILING DATE: 2000-02-25
; PRIOR FILING DATE: 60/122,156
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2440
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (294)...(1706)
US-09-513-007-1

Query Match
Best Local Similarity 50.1%; Score 685.4; DB 4; Length 2440;
Matches 1021; Conservative 0; Mismatches 326; Indels 90; Gaps 5;

Qy 1 ATGGGCTCTCCACCGTGCCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
Db 294 ATGGGCTCTCCACCGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 353
Qy 61 GGAATATACCCCTCAGGGGTTATGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 354 GATGTGTACCCCGCAGGGGTTTCAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 413
Qy 121 GATAGTGTGCTGCCCAAGGAAATATATCCACCTCAAAATAAATGATGCTGCTGCTGCTGCT 180
Db 414 GAGAGTCCCTGCTCCCAAGGAAATATATCCACCTCAAAATAAATGATGCTGCTGCTGCTGCT 473
Qy 181 AAGTGCACAAAGAACTACTTGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 474 AAGTGCACAAAGTACTTGTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
Qy 241 TGCAGGAGTGTGAGAGCGCTCTTCCACCTTCCAGAAACCACTGCTGCTGCTGCTGCTGCTG 300
Db 534 TGCAGGAGTGTGAGAGCGCTCTTCCACCTTCCAGAAACCACTGCTGCTGCTGCTGCTGCTG 593
Qy 301 AGCTGCTCAAAATCCGAAAGAAATGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 360
Db 594 AGCTGCTCAAGTCCGAGGAGAAATGTTCCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 653
Qy 361 CGGACACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 654 CGGACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713
Qy 421 TCCAGTCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 714 TCCAGTCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 773
Qy 481 AAACAGAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 774 AGACAGAACCCATCTGCCATGCCATATGGCTTCTTCTTAAGGCGCCCAAGTGCATC 833
Qy 541 TCCGTGTAGTACTGTAGAAAGCGTGGAGTGCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 834 TCCGTGTAGTACTGTAGAAAGCGTGGAGTGCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 890
Qy 601 AATGTTAAGGCACTGAGGACTCAGGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 891 ACTGGTAAAGACTCTCAGGACCCAGGCACTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 950
Qy 661 GGTCTTGGCTTTTATCCCTCCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 951 GGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1010
Qy 721 TCCAGTCTACTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 1011 CCCAAGCTCTACTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1070
Qy 781 GGAATCTACTAAGCCCTGCGCCCAACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 1071 CTCCT-----GGTCCCGGCGCCCGGCTTCAACCCCACTGCTGCTGCTGCTGCTGCTGCT 1121

QY	241	TGCAGGAGTGTGAGAGCGGCTCCTTCACGGCTTCAGAAACCACTCTCAGACACTGCCTC	300
Db	1845	TGCAGGAGTGTGAGAGCGGCTCCTTCACGGCTTCAGAAACCACTCTCAGACACTGCCTC	1904
QY	301	AGCTGCTCCAAATGCCGAAGGAATGGGTCAAGTGGATCTCTCTTGTGCACAGTGGAC	360
Db	1905	AGCTGCTCCAAATGCCGAAGGAATGGGTCAAGTGGATCTCTCTTGTGCACAGTGGAC	1964
QY	361	CGGGACACCTGTGTGGCTGCAGGAAGACCACTACCGCATTTATTTGGAGTGAACCTT	420
Db	1965	CGGGACACCTGTGTGGCTGCAGGAAGACCACTACCGCATTTATTTGGAGTGAACCTT	2024
QY	421	TTCCAGTGTCTCAATTTGCAGCCTCTGCCTCAATTTGGACCGTGCACCTCTCTGCCAGGAG	480
Db	2025	TTCCAGTGTCTCAATTTGCAGCCTCTGCCTCAATTTGGACCGTGCACCTCTCTGCCAGGAG	2084
QY	481	AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTAAGAGAAACGAGTGTGC	540
Db	2085	AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTAAGAGAAACGAGTGTGC	2144
QY	541	TCCTGTAGTAACGTGTAGAAACCGTGGAGTGCACGAAGTTGTTCCTACCCAGATTGAG	600
Db	2145	TCCTGTAGTAACGTGTAGAAACCGTGGAGTGCACGAAGTTGTTCCTACCCAGATTGAG	2204
QY	601	AATGTTAAGGGCACTGAGGACTCAGGCACCACAG	634
Db	2205	AATGTTAAGGGCACTGAGGACTCAGGCACCACAG	2238

RESULT 14

RECORD # 4
 ; Sequence 47, Application US/08050319B
 ; Patent No. 5633145
 ; GENERAL INFORMATION:
 ; APPLICANT: M. Feldmann, P.W. Gray,
 ; APPLICANT: M.J.C. Turner, F.M. Brennan
 ; TITLE OF INVENTION: Modified human TNFalpha (Tumor
 ; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Reed & Robbins
 ; STREET: 635 Bryant Street
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/050,319B
 ; FILING DATE: 10-May-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Robbins, Roberta L.
 ; REGISTRATION NUMBER: 33,208
 ; REFERENCE/DOCKET NUMBER: 5150-0030
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 617-8999
 ; TELEFAX: (415) 327-3231
 ; INFORMATION FOR SEQ ID NO: 47:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 600 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..597

US-08-050-319B-47

Query Match	43.48;	Score 593.6;	DB 1;	Length 600;
Best Local Similarity	99.34;	Pred. No. 3.4e-133;		
Matches 596;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGGGCGCTCCACCGTCCCTGACCTGCTGCTGCGCACTGGTGCTCTCGAGCTGCTTGGTG	60	
Db	1	ATGGGCGCTCTCCACCGTCCCTGACCTGCTGCTGCGGCTGGTGCTCTCGAGCTGCTTGGTG	60	
Qy	61	GGAATATACCCCTCAGGGGTATTGGACTGGTGCCTCACCTTAGGGACAGGGAGAAGAGA	120	
Db	61	GGAATATACCCCTCAGGGGTATTGGACTGGTGCCTCACCTTAGGGACAGGGAGAAGAGA	120	
Qy	121	GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCTCAAAATATTCGATTGCTGTACC	180	
Db	121	GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCCTCAAAATATTCGATTGCTGTACC	180	
Qy	181	AASTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGACAGATACGGAC	240	
Db	181	AASTGCCACAAAGGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGGACAGATACGGAC	240	
Qy	241	TGCAGGAGTGTGACAGCGGCTCCTTCAACCGCTTCAGAAACACACTCAGACACTGCCTC	300	
Db	241	TGCAGGAGTGTGACAGCGGCTCCTTCAACCGCTTCAGAAACACACTCAGACACTGCCTC	300	
Qy	301	AGCTGCTCCAAATCCGAAAGAAATGGTTCAGTGGAGATCTCTCTTGCACAGTGGAC	360	
Db	301	AGCTGCTCCAAATCCGAAAGAAATGGTTCAGTGGAGATCTCTCTTGCACAGTGGAC	360	
Qy	361	CGGGACACCGTGTGTGGCTGCAGGAAGAACACAGTACCGGCATTTATGGAGTGAACACCTT	420	
Db	361	CGGGACACCGTGTGTGGCTGCAGGAAGAACACAGTACCGGCATTTATGGAGTGAACACCTT	420	
Qy	421	TTCCAGTGTCTCAATTTGCAGGCTCTGCCTCAATGGGACCGTGCACCTCTCTCTGCCAGGAG	480	
Db	421	TTCCAGTGTCTCAATTTGCAGGCTCTGCCTCAATGGGACCGTGCACCTCTCTCTGCCAGGAG	480	
Qy	481	AAACAGAACACCGTGTGCACCTGGCATCGAGGTTTCTTCTAAAGAGAAACAGTGTCTC	540	
Db	481	AAACAGAACACCGTGTGCACCTGGCATCGAGGTTTCTTCTAAAGAGAAACAGTGTCTC	540	
Qy	541	TCCTGTAGTAACTGTAGAAAGCGCTGGAGTGCAGGAAGTTGTGCTTACCCAGATTGAG	600	
Db	541	TCCTGTAGTAACTGTAGAAAGCGCTGGAGTGCAGGAAGTTGTGCTTACCCAGATTGAG	600	

RESULT 15

```

RES001 13
US-08-465-982-47
; Sequence 47, Application US/08465982
; Patent No. 5863786
; GENERAL INFORMATION:
; APPLICANT: M. Feldmann, P.W. Gray,
; APPLICANT: M.J.C. Turner, F.M. Brennan
; TITLE OF INVENTION: Modified human TNFalpha (Tumor
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reed & Robbins
; STREET: 635 Bryant Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,982
; FILING DATE:
; CLASSIFICATION:

```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,319
; FILING DATE: 10-May-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Robbins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 5150-0030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 600 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..597
; US-08-465-982-47

Query Match      43.4%; Score 593.6; DB 2; Length 600;
Best Local Similarity 99.3%; Pred. No. 3.4e-133;
Matches 596; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGGCCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTCGAGCTGTGGTG 60
Db 1 ATGGCCCTCTCCACCGTGCCTGACCTGCTGCTGCCACTGGTGCTCCTCGAGCTGTGGTG 60
QY 61 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTACCTAGGGGACAGGAGAGAGA 120
Db 61 GGAATATACCCCTCAGGGGTTATTGGACTGGTCCCTACCTAGGGGACAGGAGAGAGA 120
QY 121 GATAGTGTGTGTCCTCCAGGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 180
Db 121 GATAGTGTGTGTCCTCCAGGAAATATATCCACCTCAAAATATTCGATTGCTGTACC 180
QY 181 AAGTCCCAAGAGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGCAGGATACGGAC 240
Db 181 AAGTCCCAAGAGAACCTACTTGTACAAATGACTGTCCAGGCCCGGGCAGGATACGGAC 240
QY 241 TGCAGGGAGTGTGAGAGCGGCTCCTTACCGCTTCAGAAACCACCTCAGACACTGCCTC 300
Db 241 TGCAGGGAGTGTGAGAGCGGCTCCTTACCGCTTCAGAAACCACCTCAGACACTGCCTC 300
QY 301 AGCTGCTCCAAATGCCGAAAGGAATGGGTGAGTGGAGATCTCTTTCACAGTGGAC 360
Db 301 AGCTGCTCCAAATGCCGAAAGGAATGGGTGAGTGGAGATCTCTTTCACAGTGGAC 360
QY 361 CGGGACACCGTGTGTGGTGTGAGGAGAACCCAGTACCGGCATTTATTGGAGTGAACCTT 420
Db 361 CGGGACACCGTGTGTGGTGTGAGGAGAACCCAGTACCGGCATTTATTGGAGTGAACCTT 420
QY 421 TTCCAGTGTTCATTTGAGGCTGTGCTCAATGGGACCGTGCACCTCTCTGCCAGGAG 480
Db 421 TTCCAGTGTTCATTTGAGGCTGTGCTCAATGGGACCGTGCACCTCTCTGCCAGGAG 480
QY 481 AAACAGAACACCGTGTGCACCTGTCATGCGATTCTTTCTAAGAGAAACGAGTGTGTC 540
Db 481 AAACAGAACACCGTGTGCACCTGTCATGCGATTCTTTCTAAGAGAAACGAGTGTGTC 540
QY 541 TCCTGTAGTAAGTGTGAAGAAAGCGTGGAGTGCAGAAAGTGTGCCTACCCAGATTGAG 600
Db 541 TCCTGTAGTAAGTGTGAAGAAAGCGTGGAGTGCAGAAAGTGTGCCTACCCAGATTGAG 600
```

Search completed: June 9, 2003, 01:14:09
Job time : 97 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2003, 01:17:59 ; Search time 185 Seconds
(without alignments)
3442.105 Million cell updates/sec

Title: US-09-899-422a-2

Perfect score: 2487

Sequence: 1 MGLSTVPDLLPLVLLELV.....DIEEALCGPALPPAPSLLR 455

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 1740770

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL-frame+ p2n.model -DEV-rlp
-Q-/cgn2_1/USPTO_spool/US09899422/runat_04062003_145738_14748/app_query.fasta_1.647
-DB-PublishedApplications.NA -QEMT-fastap -SUFFIX-rnpb -MINMATCH-0.1
-LOOPECI-0 -LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -LOCALALIGN-200 -THR_SCORE-pct -THR_MAX-100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEADSIZE-500 -MINLEN-0
-MAXLEN-2000000000 -USER-US09899422 -ECGN_1_1_80 -runat_04062003_145738_14748
-NCPU-6 -ICPU-3 -NO_MMAB -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100
-LONGLOG -DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5
-FGAPOP-6 -FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

Database : PublishedApplications.NA.*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2487	100.0	1368	9 US-09-898-234-1	Sequence 1, Appli
2	2487	100.0	1368	9 US-09-899-429A-1	Sequence 1, Appli
3	2487	100.0	1368	9 US-09-792-356-1	Sequence 1, Appli
4	2487	100.0	1368	10 US-09-899-422-1	Sequence 1, Appli

5	2487	100.0	2111	10 US-09-880-107-2360	Sequence 2360, Ap
6	2487	100.0	2141	9 US-09-898-234-16	Sequence 16, Appl
7	2487	100.0	2141	9 US-09-899-429A-26	Sequence 26, Appl
8	2487	100.0	2141	9 US-09-792-356-16	Sequence 16, Appl
9	2487	100.0	2141	10 US-09-899-422-16	Sequence 16, Appl
10	2487	100.0	2175	12 US-10-120-397-1	Sequence 1, Appli
11	2481	99.8	1568	9 US-10-352-408-3	Sequence 3, Appli
12	2069	83.2	1334	9 US-09-898-234-11	Sequence 11, Appl
13	2069	83.2	1334	9 US-09-792-356-11	Sequence 11, Appl
14	2069	83.2	1334	10 US-09-899-422-11	Sequence 11, Appl
15	2055	82.6	1334	9 US-09-899-429A-21	Sequence 21, Appl
16	1563	62.9	2130	10 US-09-917-800A-1601	Sequence 1601, Ap
17	1550.5	62.3	2173	9 US-09-898-234-14	Sequence 14, Appl
18	1550.5	62.3	2173	9 US-09-899-429A-24	Sequence 24, Appl
19	1550.5	62.3	2173	9 US-09-792-356-14	Sequence 14, Appl
20	1550.5	62.3	2173	10 US-09-899-422-14	Sequence 14, Appl
21	1517	61.0	2440	10 US-09-970-532-1	Sequence 1, Appli
22	1192	47.9	633	9 US-09-899-429A-7	Sequence 7, Appli
23	1141	45.9	603	9 US-09-899-429A-13	Sequence 13, Appl
24	1117.5	44.9	600	9 US-09-899-429A-11	Sequence 11, Appl
25	1066.5	42.9	570	9 US-09-899-429A-17	Sequence 17, Appl
26	1051	42.3	549	9 US-09-899-429A-9	Sequence 9, Appli
27	1016	40.9	1301	10 US-09-756-186-7	Sequence 7, Appli
28	1000	40.2	519	9 US-09-899-429A-15	Sequence 15, Appl
29	995.5	40.0	1147	10 US-09-756-186-5	Sequence 5, Appli
30	992	39.9	516	9 US-09-899-429A-19	Sequence 19, Appl
31	941	37.8	483	9 US-09-898-234-3	Sequence 3, Appli
32	941	37.8	483	9 US-09-899-429A-3	Sequence 3, Appli
33	941	37.8	483	9 US-09-792-356-3	Sequence 3, Appli
34	941	37.8	483	9 US-09-882-735-1	Sequence 1, Appli
35	941	37.8	483	10 US-09-899-422-3	Sequence 3, Appli
36	941	37.8	483	10 US-09-907-263-1	Sequence 1, Appli
37	941	37.8	486	9 US-09-899-429A-5	Sequence 5, Appli
38	909.5	36.6	1674	9 US-09-359-595-12	Sequence 12, Appl
39	870.5	35.0	1202	10 US-09-756-186-3	Sequence 3, Appli
40	852	34.3	1049	10 US-09-756-186-1	Sequence 1, Appli
41	843	33.9	479	9 US-10-043-487-100	Sequence 100, App
42	790	31.8	507	9 US-09-911-904-129	Sequence 129, App
43	766.5	30.8	5870	10 US-09-838-718A-8	Sequence 8, Appli
44	738.5	29.7	543	10 US-09-970-532-3	Sequence 3, Appli
45	638	25.7	339	9 US-09-882-735-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-898-234-1
; Sequence 1, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98/385-1
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1368

```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
;
; NAME/KEY: CDS
; LOCATION: (1)..(1368)
; NAME/KEY: sig_peptide
; LOCATION: (1)..(87)
; NAME/KEY: misc_feature
; LOCATION: (88)..(120)
;
; OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
; OTHER INFORMATION: extracellular proteases following secretion.
;
; NAME/KEY: misc_feature
; LOCATION: (606)..(633)
;
; OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
; OTHER INFORMATION: extracellular proteases following secretion.
;
; US-09-898-234-1

```

Alignment Scores:		
Pred. No.:	5.82e-251	1368
Score:	2487.00	455
Percent Similarity:	100.00%	0
Best Local Similarity:	100.00%	0
Query Match:	100.00%	0
DB:	9	0
	Length:	
	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

US-09-899-422A-2 (1-455) x US-09-898-234-1 (1-1368)

QY	361	AlaValValIGluAsnValProProLeuAaGTPDLYSGluPheValAArgArgLeuGlyLeu	380
Db	1081	GCGCGTGTGGAGAACGTGCCCGGTTGCGGTGAAGAATAATCTGCGGGGCGCTAGGCGCTG	1140
QY	381	SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln	400
Db	1141	AGGCACACAGATCATCGCTGGAGCTGTCAACAGGGCGCTGCTTGGCGAGGCGCAA	1200
QY	401	TyrSerMetLeuAlaThrTrpArgArgThrProArgArgGluAlaThrLeuGluLeu	420
Db	1201	TACAGCATGCTGGCGACCTGGAGCGCGCACGCCGCGGCGAGCCACGCTGGAGCTG	1260
QY	421	LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluGluAla	440
Db	1261	CTGGAGCGGTGTCGCGACATGGACCTGCTGGGTGCTGTGGAGGACATCGAGGAGCG	1320
QY	441	LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg	455
Db	1321	CTTTGGGGCCCCGCCGCCCTCCGCCCGCGCCAGTCTTCTCAGA	1365

RESULT 2

US-09-899-429A-1

: Sequence 1, Application US/09899429A

: Patent No. US20020169118A1

: GENERAL INFORMATION:

: APPLICANT: Hauptmann, Rudolph

: APPLICANT: Himmler, Adolph

: APPLICANT: Maurer-Fogy, Ingrid

: APPLICANT: Stratowa, Christian

: TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for

: TITLE OF INVENTION: Them

: FILE REFERENCE: 98-385-J

: CURRENT APPLICATION NUMBER: US/09/899,429A

: CURRENT FILING DATE: 2001-07-03

: PRIOR APPLICATION NUMBER: 09/792,356

: PRIOR FILING DATE: 2000-02-23

: PRIOR APPLICATION NUMBER: 08/477,639

: PRIOR FILING DATE: 1955-06-07

: PRIOR APPLICATION NUMBER: 08/383,676

: PRIOR FILING DATE: 1995-02-01

: PRIOR APPLICATION NUMBER: 08/153,287

: PRIOR FILING DATE: 1993-11-17

: PRIOR APPLICATION NUMBER: 07/821,750

: PRIOR FILING DATE: 1992-01-02

: PRIOR APPLICATION NUMBER: 07/511,430

: PRIOR FILING DATE: 1990-04-20

: NUMBER OF SEQ ID NOS: 97

RESULT 2

US-09-899-429A-1
; Sequence 1, Application US/09899429A

Patent No. US20020169118A1
GENERAL INFORMATION:

APPLICANT: Hauptmann, Rudolph

APPLICANT: Himmeler, Adolph

APPLICANT: MAURER-FOGY, Ingrid

APPLICANT: Stratowa, Christian

· TITLE OF INVENTION: THEM

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

; CURRENT APPLICATION NUMBER: US/09/899,429A

; CURRENT FILING DATE: 2001-07-03

; PRIOR APPLICATION NUMBER: 09/792,356

; PRIOR FILING DATE: 2000-02-23

; PRIOR APPLICATION NUMBER: 08/477,639

; PRIOR FILING DATE: 1955-06-07
 ; PRIOR APPLICATION NUMBER: 08/383 676

; PRIOR APPLICATION NUMBER: 08/383,676
 ; PRIOR FILING DATE: 1995-02-01

; PRIOR FILING DATE: 1993-02-01
 ; PRIOR APPLICATION NUMBER: 08/153,287

; PRIOR FILING DATE: 1993-11-17

; PRIOR APPLICATION NUMBER: 07/821,750

; PRIOR FILING DATE: 1992-01-02

; PRIOR APPLICATION NUMBER: 07/511,430

; PRIOR FILING DATE: 1990-04-20
 ;
 ; NUMBER OF SEQ ID NOS: 07

; NUMBER OF SEQ ID NOS: 5 /

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1
 LENGTH: 1368
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1365)
 NAME/KEY: sig_peptide
 LOCATION: (1)..(87)
 NAME/KEY: misc_feature
 LOCATION: (88)..(120)
 OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
 OTHER INFORMATION: extracellular proteases following secretion
 NAME/KEY: misc_feature
 LOCATION: (606)..(633)
 OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
 OTHER INFORMATION: extracellular proteases following secretion
 US-09-899-429A-1

Alignment Scores:
 Pred. No.: 5,82e-251 Length: 1368
 Score: 2487.00 Matches: 455
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-899-422A-2 (1-455) x US-09-899-429A-1 (1-1368)

QY 1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuLeuVal 20
 DB 1 ATGGGCTCTCCACCGTGGCTGCTGCTGCTGCCACTGGTCTCTGGAGCTGTGGTG 60
 QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
 DB 61 GGAAATATACCCCTCAGGGGTATTGACATGGTCCCTTCACTAGGGGACAGGGAAGA 120
 QY 41 AspSerValCysProGlnGlyTyrIleHisProGlnAsnSerIleCysCysThr 60
 DB 121 GATAGTGTGTGTCCTCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGCTGACC 180
 QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
 DB 181 AAGTGCACAAAGGAAACCTACTTGTACATGACTGTCCAGGCCCGGGGAGATACGGAC 240
 QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
 DB 241 TGCAGGGAGTGTGAGAGGGCTCTTCACCGCTTCAGAAACACCTCAGACACTGCCTC 300
 QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
 DB 301 AGCTGCTCCAAATGCCGAAAGGAAATGGGTGAGTGGAGATCTCTTCTTGACAGTGGAC 360
 QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
 DB 361 CGGGACACCGTGTGGTGCAGGAAGAACACCTACCGGCATTATTGGAGTGAACACCT 420
 QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
 DB 421 TTCAGTGTCTCAATTCGACCTCTGCTCAATGGGACCGTGCACCTCTCTCCACAGGAG 480
 QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGlyCysVal 180
 DB 481 AAACAGAACACCGTGTGCACCTGCCATGCCATGCAAGTTTCTTCTAAGAGAAACAGAGTGTGTC 540
 QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
 DB 541 TCCTGTAGTAACCTGTGAAGAAACCCCTGGAGTGCACGAAGTGTGCTACCCCAATGAG 600
 QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
 DB 601 AATGTTAAGGGCACTAGGAGCTCAGGCACACAGTGTGTGGCCCTGGTCAATTTCTTT 660

QY 221 GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTyrLys 240
 DB 661 GGTCCTTTGCTTTTATCCCTCTCTTCATTGGTTTAAATGATCGCTACCAACGGTGAAG 720
 QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGluLeuGlu 260
 DB 721 TCCAGCTCTACTCCATTGTTGGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 780
 QY 261 GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
 DB 781 GGAACCTACTACTAAGCCCTGGCCCAACCCAAAGCTTCAGTCCCACTCCAGGCTTACC 840
 QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrTyrThr 300
 DB 841 CCCACCTGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 QY 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 320
 DB 901 CCGGTGACTGTCCTCAACTTTCGGCTCCCGCAGAGAGTGGCACCACCTATCAGGGG 960
 QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
 DB 961 GCTGACCCCTACTCTCGACAGCCCTCGCTCGACCCCTCCCAACCCCTTCAAGAG 1020
 QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
 DB 1021 TGGGAGGACAGCCGCCACCAAGCCACAGAGCCCTAGACACTGATGACCCCGGAGCTGTAC 1080
 QY 361 AlaValValGluAsnValProProLeuArgTyrTrpLysGluPheValArgArgLeuGlu 380
 DB 1081 GCGTGTGGAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
 QY 381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
 DB 1141 AGCAGCACAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 QY 401 TyrSerMetLeuAlaThrTrpArgArgTyrProArgArgGluAlaThrLeuGluLeu 420
 DB 1201 TACAGCATGCTGGCGACCTGGAGCGGCACCGCGCGGCGGAGGCCAGCTGGAGCTG 1260
 QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
 DB 1261 CTGGGACGGTGTCTCGGACATGAGCTGCTGGCTGCTGGAGACATCGAGGAGCGG 1320
 QY 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
 DB 1321 CTTTGGGGCCCGCCCTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 1365

RESULT 3

US-09-792-356-1

; Sequence 1, Application US/09792356
 ; Publication No. US20020183485A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hauptmann, Rudolph
 ; APPLICANT: Himmler, Adolph
 ; APPLICANT: Maurer-Fogy, Ingrid
 ; APPLICANT: Strata-Towa, Christian
 ; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
 ; TITLE OF INVENTION: them
 ; FILE REFERENCE: 98,385-G
 ; CURRENT APPLICATION NUMBER: US/09/792,356
 ; PRIOR FILING DATE: 2001-08-17
 ; PRIOR APPLICATION NUMBER: 08/477,639
 ; PRIOR FILING DATE: 1995-06-07
 ; PRIOR APPLICATION NUMBER: 08/383,676
 ; PRIOR FILING DATE: 1995-02-01
 ; PRIOR APPLICATION NUMBER: 08/153,287
 ; PRIOR FILING DATE: 1993-11-17
 ; PRIOR APPLICATION NUMBER: 07/821,750
 ; PRIOR FILING DATE: 1992-01-02
 ; PRIOR APPLICATION NUMBER: 07/511,430
 ; PRIOR FILING DATE: 1990-04-20

ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981a1 M58286
US-09-880-107-2360

Alignment Scores:
Pred. No.: 1,12e-250 Length: 2111
Score: 2487.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-899-422a-2 (1-455) x US-09-880-107-2360 (1-2111)

QY 1 MetGlyLeuSerThrValProAspLeuLeuValLeuLeuLeuVal 20
DB 187 ATGGCCCTCTCCACCGTGCCTGACCTGCTGCTGCGCTGGTGTGTG 246
QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
DB 247 GGAATATACCCCTCAGGGGTTATTGGACTGCTCCCTCACCTAGGGGACAGGAGAGA 306
QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
DB 307 GATAGTGTGTGCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGTGCTGTACC 366
QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
DB 367 AAGTGCACAAAGAACCTACTTGTACAACTGCTCAGCGCCGGGCGAGATACGGAC 426
QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
DB 427 TGCAGGGAGTGTGAGCGGCTCTCTACCCGCTTCAGAAACACCACTCAGACACTGCCTC 486
QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGlnIleSerSerCysThrValAsp 120
DB 487 ACCTGCTCCAAATGCCGAAGAAATGGGTGAGTGGAGATCTCTTGTGCACAGTGAC 546
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
DB 547 CGGACACCGTGTGGCTGCAGGAAGAACCACTACCGCATATTGGAGTGAACACCT 606
QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
DB 607 TTCAGTGTCTCAATTCAGCTCTGCCTCAATGGACCGTGCACCTCTCTCTGCAGAG 666
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysVal 180
DB 667 AAACAGAACCGTGTGCACCTGCCATGCAGGTTCTTCTTAAGAGAAACAGTGTGTC 726
QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
DB 727 TCCTGTAGTAAGTAAAGAAAGCTGGAGTGCAGGAAGTGTGCTTACCCACAGATTGAG 786
QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhephe 220
DB 787 AATGTTAAGGCACGTGAGGACTCAGGCACCACTGCTGTGTGCCCTGGTCAATTTCTTT 846
QY 221 GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
DB 847 GCTCTTGGCCCTTTATCCCTCTCTTTCATGTTGTTTAAATGATATCTACCAACGGTGAAG 906
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyLeuGlu 260
DB 907 TCCAAGCTCTACTCCTGTTTGTGGAAATCGACACTGAAAGAGGGGGAGCTTGAA 966
QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
DB 967 GGAATCTACTAAGCCCTTGGCCCAACACCAAGCTTCAGTCCCACTCCAGGCTTCACC 1026
QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrTyrThr 300

DB 1027 CCCACCCCTGGGCTTCAGTCCCGTGCCTCCAGTTCCACCTTCCAGCTCCAGCTCCACCTATACC 1086
QY 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 320
DB 1087 CCCGCTGACTGTCCCAACTTTGCGGCTCCCGCGAGAGGTGGCACCACCCCTATCAGGGG 1146
QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
DB 1147 GCTGACCCCATCTTGGACAGCCTCGCTCCGACCCATCCCAACCCCTTCAGAAAG 1206
QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
DB 1207 TGGAGGACAGCGCCCAACAGCCACAGCTAGACACTGATGACCCGCGCCAGCTGTGAC 1266
QY 361 AlaValValGluAsnValProProLeuArgTyrLysGluPheValArgArgLeuGlyLeu 380
DB 1267 GCCGTGTGGAGAACGTGCCCTGCTGCGTGGAGGAATTCGTGCGGCGCTAGGGCTG 1326
QY 381 SerAspHisGluIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
DB 1327 AGCGACCAAGAGATCGATCGCTGGAGCTGCAGAACCGGCGCTGCTGCGGAGCGCAA 1386
QY 401 TyrSerMetLeuAlaThrTrpArgArgThrProArgArgGluAlaThrLeuGluLeu 420
DB 1387 TACAGCATGCTGGCGACCTGGAGGCGGCGCACCGCGGCGGAGGCGCACCTGGAGCTG 1446
QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
DB 1447 CTGGAGCGCTGCTCCGACATGACCTGCTGGCTGCTGGAGGACATCGAGGAGCG 1506
QY 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
DB 1507 CTTTGGCGCGCGCGCTCCCGCGCGCGCTCTCTCTCAGA 1551

RESULT 6

US-09-898-234-16
; Sequence 16, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Pogny, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2141
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213)..(1580)
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
; OTHER INFORMATION: ITNF-R2
US-09-898-234-16
Alignment Scores:
Pred. No.: 1.14e-250 Length: 2141

QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
DB 273 GGAATATACCCCTCAGGGGTATTGGACATGGTCCCTCACCCTAGGGACAGGGAGAGA 332
QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
DB 333 GATAGTGTGTCCCAAGAAATATATCCACCCTCAAAATAATTCGATTGCTGTACC 392
QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
DB 393 AAGTGCACAAAGGAACCTACTTGTACAATGACTGCCAGGGCCGGCGAGGATACGGAC 452
QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
DB 453 TGCAGGAGTGTGAGAGCGGCTCTTCACCGCTTCAGAAACACACCTCAGACTGCCCT 512
QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
DB 513 AGCTGCTCCAAATGCCAAAGGAATGGGTGACGTGAGATCTCTTCTTGCACAGTGGAC 572
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
DB 573 CGGACACACCGTGTGGCTGCAGGAAGAACACAGTACCGGCATTATTGGAGTGAACCTT 632
QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
DB 633 TTCAGTGTCTCAATTCAGAGCTCTGCCTCAATGGGACCGTGCACCTCTCCTGCCAGGAG 692
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysVal 180
DB 693 AAACAGACACCGTGTGCACCTGCCATGCCATGGAGTTCTTCTTAAGAGAAACAGTGTGC 752
QY 181 SerCysSerAsnCysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
DB 753 TCCTGTAGTAACCTGTAAAGAAAGCCCTGGAGTGCACGAAGTTGTGCCTACCCAGATTGAG 812
QY 201 AsnValIleGlyThrGluAspSerGlyThrValLeuLeuProLeuValIlePhePhe 220
DB 813 AATGTTAAGGGCACTGAGGACTCAGGACACACAGTGTGTGCCCTGGTCAATTTCTTT 872
QY 221 GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTyrLys 240
DB 873 GGTCTTTGCTTTTATCCCTCCCTCTTCATTGGTTTAAATGATGCTACCAACCGTGAAG 932
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyGluLeuGlu 260
DB 933 TCCAAGCTCTACTCCATTGTTGTGGGAATCGACACCTGAAAGAGGGGAGCTTGAA 992
QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
DB 993 GGAACCTACTAAGCCCTTGGCCCAACCCCAAGCTTCAGTCCCACTCCAGGCTTCACC 1052
QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrTyrThr 300
DB 1053 CCCACCTGGGCTTACGTCCGTCGCGCCAGTTCCACCTTCACCTCCAGCTCCACCTATACC 1112
QY 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProTyrGlnGly 320
DB 1113 CCGGCTGACTGTCCCACTTGGCGCTCCCGCAGAGAGGTGGCACCACCCATCATCGGGG 1172
QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
DB 1173 GCTGACCCCACTCTGGACAGCCCTCGCCTCCGACCCCACTCCCAACCCCTTCAGAAG 1232
QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
DB 1233 TGGAGGACAGCGCCACAGGACACAGAGCCTAGACACTGATGACCCCGGAGCGCTGAC 1292
QY 361 AlaValValGluAsnValProProLeuArgTyrTrpLysGluPheValArgArgLeuGlyLeu 380
DB 1293 GCGGTGTGGAGAACCTGCCCCGTTGCGTGGAGGAATTCGTGGCGGCCCTAGGCGCTG 1352
QY 381 SerAspHisGluIleAspArgLeuGluLeuAsnGlyArgCysLeuArgGluAlaGln 400

DB 1353 AGGACACACAGATCCATCGCTGGAGCTGCAGACGGGCGCTGCCTCGCGAGGCGCAA 1412
QY 401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
DB 1413 TACAGCATGCTGGCGACCTGGAGGCGCGCACCGCGCGGAGCCAGCTGGAGCTG 1472
QY 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
DB 1473 CTGGGAGCGGTGCTCCGCGACATGGACCTGCTGGCTGCTGGAGGACATCGAGAGCG 1532
QY 441 LeuCysGlyProAlaAlaLeuProAlaProSerLeuLeuArg 455
DB 1533 CTTTGGCGCCCGCCGCTCCCGCGCGCGCGCGCTTCTCTCAGA 1577

RESULT 9
US-09-899-422-16
; Sequence 16, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2141
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213)..(1580)
; OTHER INFORMATION: Description of Artificial Sequence: human TNF-R in
; OTHER INFORMATION: TNF-R2
US-09-899-422-16

Alignment Scores:
Pred. No.: 1-14e-250 Length: 2141
Score: 2487.00 Matches: 455
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Caps: 0

US-09-899-422A-2 (1-455) x US-09-899-422-16 (1-2141)

QY 1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuLeuVal 20
DB 213 ATGGGCTCTCCACCGTCCCTGACCTGCTGCCACTGTGTCTCTCTGGAGCTGTGTG 272
QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
DB 273 GGAATATACCCCTCAGGGGTATTGGACATGGTCCCTCACCCTAGGGACAGGGAGAGA 332
QY 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
DB 333 GATAGTGTGTGTCCCAAGAAATATATCCACCCTCAAAATAATTCGATTGCTGTACC 392

Db 61 GGAATATACCCCTCAGGGGTATTTGGACTGGTCCCTCACCTAGGGGACAGGAGAGAGA 120
Qy 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
Db 121 GATAGTGTGTGTCCTCCCAAGGAATATATCCACCTCAAATAATTCGATTGCTGTACC 180
Qy 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
Db 181 AAGTCCCAACAAGGAACCTACTGTACATGACTGTCCAGGCGCGGGCAGGATACGGAC 240
Qy 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db 241 TCCAGGGAGTGTGAGCGGCTCTTCCACCGCTTCAGAAACACCTCAGACATGCGCTC 300
Qy 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db 301 AGCTGCTCCAAATGCCGAAGGAATGGTCCAGGTGGAGATCTCTTCTGCACAGTGAC 360
Qy 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
Db 361 CGGGACACCGTGTGTGGCTGCAGGAAGAACAGTACCGGCATATTATGGAGTGAACACCT 420
Qy 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 421 TTCAGTCTCAATGTGAGCTCTGCTCAATGGGACCGTGCACCTCTCTCGCCAGGAG 480
Qy 161 LysGlnAsnThrValCysThrCysHisAlaGlyPheLeuArgGluAsnGluCysVal 180
Db 481 AAACAGAACACCGTGTGCACCTGCCATGCAGGTTTCTTCTTAAGAGAAACAGGTGTCTC 540
Qy 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 541 TCCTGTACTAAGTGTAAAGAAAGCGTGGAGTGCAGAAAGTGTGCTTACCCAGATTGAG 600
Qy 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
Db 601 AATGTTAAGGACACTGAGGACTCAGGCACACAGTGTGTGCCCCCTGGTCAATTTCTTT 660
Qy 221 GlyLeuCysLeuLeuSerLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
Db 661 GGTCTTTGCCCTTTATCCCTCTCTTCATTGTTTAAAGTTATCGTACCAACGGGTGAAG 720
Qy 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGlyCyluLeuGlu 260
Db 721 TCCAAGCTCTACTCCATGTTGTGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 780
Qy 261 GlyThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 781 GGACTACTACTAAGCCCTCGGCCCAACCAAGCTTCAGTCCCACTCCAGGCTTACC 840
Qy 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerThrTyrThr 300
Db 841 CCCACCTGGGCTTCAGTCCCGTGCACATTCACCTTCACCTCCAGCTCCACCTATACC 900
Qy 301 ProGlyAspCysProAsnPheAlaAlaProArgGluValAlaProProTyrGlnGly 320
Db 901 CCCGTGACTCTCCCAACTTTGCGGCTCCCGCAGAGAGGTGGCACCACTATCAGGGG 960
Qy 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
Db 961 GCTGACCCCACTTTCGAGACAGCCCTCGCCCTCCGACCCCAATCCCAACCCCTTCAGAG 1020
Qy 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaThrLeuTyr 360
Db 1021 TGGGAGGACAGCGCCCAACCCACAGAGCCCTAGACACTGATACCCCGCGCAGCTGTAC 1080
Qy 361 AlaValValGluAsnValProProLeuArgTrpLysGluPheValArgArgLeuGlyLeu 380
Db 1081 GCCGTGTGTGAAGACGTGCCCGCTGGCGTGGGAAGAAATTCGTGCGCGCGCTAGGGCTG 1140
Qy 381 SerAspHisGluIleAspArgLeuLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
Db 1141 ACCGACCAAGAGATCGATCGGCTGGAGTGCAGAACGGGCGCTGCTCGCGGAGCGCAA 1200

Qy 401 TyrSerMetLeuAlaThrTyrArgArgArgThrProArgArgGluAlaThrLeuGluLeu 420
Db 1201 TACAGCATGCTGGGACCTGGAGGGCGGCACCGCGCGGAGGCCACCTGGAGCTG 1260
Qy 421 LeuGlyArgValLeuArgAspMetAspLeuLeuGlyCysLeuGluAspIleGluAla 440
Db 1261 CTGGACACGCTGCTCCGCGACATGGACCTGCTGGGCTGCTGGAGGACATCGAGAGCG 1320
Qy 441 LeuCysGlyProAlaAlaLeuProProAlaProSerLeuLeuArg 455
Db 1321 CTTTGGCGCGCGCGCGCTCCGCGCGCGCGCGCTCTCTCAGA 1365

RESULT 12

US-09-898-234-11
; Sequence 11, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213)..(1325)
; OTHER INFORMATION: Description of Artificial Sequence: cDNA insert of
; OTHER INFORMATION: lambdaTNF-BP15 and pTNF-BP15 vectors
US-09-898-234-11

Alignment Scores:
Pred. No.: 3,67e-207 Length: 1334
Score: 2069.00 Matches: 374
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.19% Indels: 0
DB: 9 Gaps: 0

US-09-899-422A-2 (1-455) x US-09-898-234-11 (1-1334)

Qy 1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGluLeuVal 20
Db 213 ATGGCCCTCTCCACCGTCCCTGACCTGCTGCTGCCACTGTGCTCTCTGGAGCTGTGGTG 272
Qy 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
Db 273 GGAATATACCCCTCAGGGGTTATTGGACTGTGCTCCCTACCTAGGGGACAGGAGAGA 332
Qy 41 AspSerValCysProGlnGlyLysTyrIleHisProGlnAsnAsnSerIleCysCysThr 60
Db 333 GATAGTGTGTGCTCCCAAGGAATAATATATCCACCTCAAAATATTCGATTTGCTGTACC 392
Qy 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80


```
QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 753 TCCTGTAGTAACCTGTAAGAAAGCCCTGGAGTGCACAGAGTTGTGCTACCCAGATTGAG 812
QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
Db 813 AATGTTAAGGCACTGAGACTCAGCACACAGTGTGTGCTCCCTGGTCAATTTCTTT 872
QY 221 GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
Db 873 GGTCTTTGCCCTTTATCCCTCCTCTTCATTTGTTAATGATCGCTACCAACGGTGGAG 932
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGluLeuGlu 260
Db 933 TCCAAAGCTACTTCCATTTGTTGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 992
QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 993 GGAAGCTACTTACCCCTCGCCCAACCCAGCTTCAGTCCCACTCCAGGCTTCACC 1052
QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrThrThr 300
Db 1053 CCCACCTGGGCTTCAGTCCGCTGCCAGTTCACCTCCAGCTCCACCTATACC 1112
QY 301 ProGlyAspCysProAsnPheAlaAlaProArgArgGluValAlaProProThrGlnGly 320
Db 1113 CCCGGTGACTGTCCCAACTTTCGGGCTCCCGCCAGAGAGTGGCACCCCTATCAGGG 1172
QY 321 AlaAspProIleLeuAlaThrAlaLeuAlaSerAspProIleProAsnProLeuGlnLys 340
Db 1173 GCTGACCCCTTCCTTGCACAGCCCTCCCTCCGACCCCTCCCAACCCCTTCAGAG 1232
QY 341 TrpGluAspSerAlaHisLysProGlnSerLeuAspThrAspProAlaThrLeuTyr 360
Db 1233 TGGGAGGACAGCGCCCAAGCACAGAGCTAGACACTGATGACCCCGCAGCGTGTAC 1292
QY 361 AlaValValGluAsnValProProLeuArgTrpLysGluPhe 374
Db 1293 GCCGTGGTGGAGAACGTGCCCGCTTGGCTGGGAAGGAATTC 1334
```

RESULT 14

```
US-09-899-422-11
; Sequence 11, Application US/09899422
; Patent No. US2002090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmeler, Adolf
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: them
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (213)..(1325)
```

```
; OTHER INFORMATION: Description of Artificial Sequence: cDNA insert of
; OTHER INFORMATION: lambdaTNF-BP15 and pTNF-BP15 vectors
US-09-899-422-11
```

Alignment Scores:

```
Pred. No.: 3,67e-207 Length: 1334
Score: 2069.00 Matches: 374
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.19% Indels: 0
DB: 10 Gaps: 0
```

US-09-899-422a-2 (1-455) x US-09-899-422-11 (1-1334)

```
QY 1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuGluLeuVal 20
Db 213 ATGGCCCTCTCCACCGTCCCTGACCTGCTGCTGCCACTGGTCTCCTGAGACTGTTGGTG 272
QY 21 GlyIleTyrProSerGlyValIleGlyLeuValProHisLeuGlyAspArgGluLysArg 40
Db 273 GGAATATACCCCTCAGGGGTTATTGGACTGCTCCCTCACCTAGGGGACAGGAGAAGA 332
QY 41 AspSerValCysProGlnGlySerThrIleHisProGlnAsnSerIleCysCysThr 60
Db 333 GATAGTGTGTGCCCAAGGAAATATATCCACCTCAAAATAATTCGATTGCTGTACC 392
QY 61 LysCysHisLysGlyThrTyrLeuTyrAsnAspCysProGlyProGlyGlnAspThrAsp 80
Db 393 AAGTCCCAAAAGGAACCTACTGTACAACTGCTCCAGGCCCGGGGAGATACGGAC 452
QY 81 CysArgGluCysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
Db 453 TGCAGGGAGTGTGAGAGCGGCTCTTCCACCGCTTCAGAAAAACCACTCAGACACTGCCTC 512
QY 101 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCysThrValAsp 120
Db 513 AGCTGCTCCAAATGCCGAAGAAATAGGTGAGTGGAGATCTCTTCTTGACACTGGAC 572
QY 121 ArgAspThrValCysGlyCysArgLysAsnGlnTyrArgHisTyrTrpSerGluAsnLeu 140
Db 573 CGGGACACCGTGTGTGGCTGCAGGAAGAACCACTACCGGCATTATTGGAGTGAACCTT 632
QY 141 PheGlnCysPheAsnCysSerLeuCysLeuAsnGlyThrValHisLeuSerCysGlnGlu 160
Db 633 TTCAGTGTCTTCAATTGCAGCTCTGCTCAATGGGACCGTGCACCTCTCTTCCAGGAG 692
QY 161 LysGlnAsnThrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180
Db 693 AAACAGACACCGTGTGCACCTGCATGACAGTTTCTTCTTAAGAAAAACAGAGTGTGTC 752
QY 181 SerCysSerAsnCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 200
Db 753 TCCTGTAGTAACCTGTAAGAAAGCCCTGGAGTGCACAGAGTTGTGCTACCCAGATTGAG 812
QY 201 AsnValLysGlyThrGluAspSerGlyThrThrValLeuLeuProLeuValIlePhePhe 220
Db 813 AATGTTAAGGCACTGAGACTCAGCACACAGTGTGTGCTCCCTGGTCAATTTCTTT 872
QY 221 GlyLeuCysLeuLeuSerLeuLeuPheIleGlyLeuMetTyrArgTyrGlnArgTrpLys 240
Db 873 GGTCTTTGCCCTTTATCCCTCCTCTTCATTTGTTAATGATCGCTACCAACGGTGGAG 932
QY 241 SerLysLeuTyrSerIleValCysGlyLysSerThrProGluLysGluGluLeuGlu 260
Db 933 TCCAAAGCTACTTCCATTTGTTGGAAATCGACACCTGAAAGAGGGGAGCTTGAA 992
QY 261 GlyThrThrThrLysProLeuAlaProAsnProSerPheSerProThrProGlyPheThr 280
Db 993 GGAAGCTACTTACCCCTCGCCCAACCCAGCTTCAGTCCCACTCCAGGCTTCACC 1052
QY 281 ProThrLeuGlyPheSerProValProSerSerThrPheThrSerSerSerThrThrThr 300
Db 1053 CCCACCTGGGCTTCAGTCCGCTGCCAGTTCACCTCCAGCTCCACCTATACC 1112
```


THIS PAGE BLANK (USPTO)